

TABLE III

		POSITION								
MOTIFS		1° anchor 1	2	3	4	5	1° anchor 6	7	8	9
DR4	preferred	FMVLIIVW	M	T		I	VSTCPALIM	MH		MH
	deleterious				W			R		WDE
DR1	preferred	MEFLIVWY			PAMQ		VMATSPIC	M		AVM
	deleterious		C	CH	FD	CWD		GDE	D	
DR7	preferred	MEFLIVWY	M	W	A		IVMSACTPL	M		IV (SEQ ID NO:3682)
	deleterious		C		G			GRD	N	G (SEQ ID NO:3683)
DR Supermotif		MEFLIVWY					VMSTACP LI			

DR3 MOTIFS	1° anchor 1	2	3	1° anchor 4	5	1° anchor 6
motif a						
preferred	LIVMFY			D		
motif b						
preferred	LIVMFAY			DNQEST		KRH

Italicized residues indicate less preferred or "tolerated" residues.

**Table IV: HLA Class I Standard Peptide Binding Affinity.**

ALLELE	STANDARD PEPTIDE	SEQUENCE	SEQ ID NO:	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	YLEPAIAKY	3606	25
A*0201	941.01	FLPSDYFPSV	3607	5.0
A*0202	941.01	FLPSDYFPSV	3608	4.3
A*0203	941.01	FLPSDYFPSV	3609	10
A*0205	941.01	FLPSDYFPSV	3610	4.3
A*0206	941.01	FLPSDYFPSV	3611	3.7
A*0207	941.01	FLPSDYFPSV	3612	23
A*6802	1072.34	YVIKVSARV	3613	8.0
A*0301	941.12	KVFPYALINK	3614	11
A*1101	940.06	AVDLYHFLK	3615	6.0
A*3101	941.12	KVFPYALINK	3616	18
A*3301	1083.02	STLPETYVRR	3617	29
A*6801	941.12	KVFPYALINK	3618	8.0
A*2402	979.02	AYIDNYNKF	3619	12
B*0702	1075.23	APRTLVL	3620	5.5
B*3501	1021.05	FPEKYAAAF	3621	7.2
B51	1021.05	FPEKYAAAF	3622	5.5
B*5301	1021.05	FPEKYAAAF	3623	9.3
B*5401	1021.05	FPEKYAAAF	3624	10

Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	Sequence	SEQ ID NO:	Binding Affinity (nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	3625	5.0
DRB1*0301	DR3	829.02	YKTIAFDDEEARR	3626	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	3627	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	3628	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	3629	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	3630	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	3631	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	3632	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	3633	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	3634	20
DRB1*1201	DR5w12	1200.05	EALIHQLKINPYVLS	3635	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	3636	3.5
DRB1*1501	DR2w2 $\beta$ 1	507.02	GRTQDENPVVHFFK NIVTPRTPPP	3637	9.1
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	3638	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT	3639	58
DRB5*0101	DR2w2 $\beta$ 2	553.01	QYIKANSKFIGITE	3640	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

SE 10070501

Table VII

HCV A01 Super Motif with Binding Information

Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101
ALGILPGYSE	1	165		10	13	93	
ALIGFGAY	2	1265		8	14	100	
AVQWIRILIAF	3	1917		11	14	100	
CLGGSRLY	4	1128	1069.62	9	11	79	0.3700
CHRWAKAVLIF	5	1190		11	11	79	
CLWIRGIFG	6	555		9	11	79	
CVIGIVIR	7	1462		8	12	86	
DEVVITLW	8	1657		9	12	86	
ETMRGCVF	9	1207		9	12	86	
ESYDRG	10	2670		8	11	79	
ETIAMTRY	11	2792		8	14	100	
ETGLTHDAIF	12	1567		11	13	93	
GLFWLGRLEF	13	1552		11	12	86	
GLSALSLHSY	14	2921	1073.03	10	11	79	0.0029
GLTHDAIF	15	1569		9	13	93	
GSSVGRQY	16	2641		8	11	79	
GLTFIRJAY	17	2063		8	11	79	
GNAGALVAF	18	1863		9	12	86	
GVAKAVLIF	19	1193		8	11	79	
GLVLAALAAV	20	1670	1174.19	9	12	86	
GVHVFEPALV	21	2639		11	14	100	
GVNIEKGVNY	22	154		11	12	86	
HLKRLIVMAY	23	696		11	11	79	
HMWIFSGIY	24	1769		11	13	93	
HLGKFGAVCW	25	1910		11	11	79	
IMAKDFVF	26	2591		8	12	86	
ILYSTIGRF	27	1296		9	12	86	
IVWDYLY	28	701		8	12	86	
KSTWVPAAY	29	1241	13.2010	9	12	86	0.0130
KVILITCGF	30	121		10	12	86	
LEANILW	31	2235		8	12	86	
LVNIGSW	32	414		8	11	79	
LIAPILAY	33	1030		8	14	100	
LIENILGGW	34	1812		9	12	86	
ILSPRGSPSW	35	97		11	11	79	
LSALSLHSY	36	2922	13.0019	9	11	79	0.8100
LSFRGSPSW	37	98		10	11	79	
LTGGAADMGY	38	126		11	12	86	
LIHDAIF	39	1570		8	13	93	
LVILAGY	40	1853		8	11	79	
MLMIDHF	41	2876		8	12	86	
NIVIMQVLY	42	700	1073.01	9	12	86	0.0980
NIPGCSFIF	43	168		10	13	93	
NICVGVIVDF	44	1460		10	12	86	
NINRRQVQKF	45	14		11	11	79	

Sequence	Gap/Alan	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0.101
RMXXRVW	46	1108		9	11	79	
PLVSTVKE	47	1295		10	11	79	
PMGLSDHRE	48	2667		11	11	79	
PSVAATLGF	49	1261		9	14	100	
PLHGPTLLY	50	1621		11	11	79	
PMXXRRE	51	1554		9	12	86	
PMXXRLFW	52	1554		10	12	86	
QIMDFSLRTE	53	1465		11	12	86	
RIHGLSAI	54	2918		8	12	86	
RLCAPTAY	55	1029	1174 18	9	12	86	
RMWVLRRLNW	56	317		10	12	86	
RMIMTHRE	57	2875		8	12	86	
RMIMTHRE	58	2875		9	12	86	
RVCERKALY	59	2621	1174 21	9	14	100	
RMFDKATY	60	156	1174 17	9	12	86	
SEKVPAAV	61	1242		8	12	86	
SVAATLGGAY	62	1262		8	14	100	
SVAATLGGAY	63	1262		11	14	100	
TIMAKRVE	64	2599		9	11	79	
TLHGPTLLY	65	1622	1073 04	10	11	79	0.0300
TLTNEIGAW	66	1811		10	12	86	
TIMAKRVE	67	2589		10	11	79	
TIMKSPVI	68	1208		8	12	86	
IVDFSLDITE	69	1466		10	12	86	
VIDLITCG	70	122		9	12	86	
VLAAIAAY	71	1671		8	12	86	
VLEKVRVY	72	157		8	12	86	
VLDIACVY	73	1852		9	11	79	
VMGSSYGF	74	2639		8	11	79	
VMGSSYGFQY	75	2639		10	11	79	
WMNRILAI	76	1920		8	14	100	
YSKQRMVE	77	2648		9	11	79	
YINVDJRVGW	78	1106		11	11	79	
YVGDCEENVF	79	276		10	12	86	

Table VIII  
HCV A02 Super Motif with Binding Information

Conservancy	Freq	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
93	13			1904	AAILRRHV	80			
86	12			1673	AALAAAYCL	81			
79	11			1250	AAQGYKVL	82			
79	11			1250	AAQGYKVLV	83			
79	11			1250	AAQGYKVLVL	84			
79	11			147	AARALAHGV	85			
79	11			147	AARALAHGVRV	86			
100	14			1264	AATLGFGA	87			
93	13			1264	AATLGFGAYM	88			
86	12			1187	AAVCTRGV	89			
79	11			1187	AAVCTRGVA	90			
79	11			1187	AAVCTRGVAK	91			
93	13			1890	AILSPGAL	92			
86	12	24.0067		1890	AILSPGALV	93	0.0014		
86	12	24.0101		1890	AILSPGALVV	94	0.0035		
100	14			150	ALAHGVRV	95			
100	14	1013.16		150	ALAHGVRVL	96	0.0037		
86	12			1737	ALGLLQTA	97			
86	12	1013.12		689	ALSTGLIHL	98	0.0160		
79	11	40.0089		1896	ALVGVVCA	99	0.0010		
79	11			1896	ALVGVVCAAA	100			
79	11			1896	ALVGVVCAAI	101			
86	12			1602	AQAPPSPWDO	102			
79	11			1251	AQGYKVLV	103			
79	11			1251	AQGYKVLVL	104			
86	12			77	AQGYKVLVL	105			
93	13			1265	ATLGFGAYM	106			
79	11			1354	ATPGSVT	107			
79	11			1596	ATVCARAQA	108			
100	14			1419	AVAYYRGL	109			
100	14	1.0486		1419	AVAYYRGLDV	110	0.0002		
79	11			1188	AVCTRGVA	111			
79	11			1188	AVCTRGVAKA	112			
79	11			1188	AVCTRGVAKAV	113			
100	14			1917	AVQWMNRL	114			
100	14	1174.09		1917	AVQWMNRLI	115	0.0001		
100	14			1917	AVQWMNRLIA	116			
93	13			1903	CAAILRRHV	117			
79	11			1530	CAWYELTPA	118			
86	12	1.0510		2941	CLRLKLGVPPL	119	0.0002		
86	12			739	CLWMMILLI	120			
79	11			1653	CMSADLEV	121			

Conservancy	Freq.	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
79	11	1.0131		1653	CMSADLEVV	122	0.0067		
79	11			1653	CMSADLEWVT	123			
79	11			1128	CTCGSSDL	124			
79	11			1128	CTCGSSDLYL	125			
79	11			1128	CTCGSSDLYLV	126			
79	11			1190	CTRGVAKA	127			
79	11			1190	CTRGVAKAV	128			
79	11			555	CTWMNSTGFT	129			
79	11	1.0487		1462	CVTQTVDFSL	130	0.0006		
86	12			1527	DAGCAWYEL	131			
79	11			1574	DAHFLSQT	132			
100	14			1855	DILAGYGA	133			
86	12			1855	DILAGYGAGV	134	0.0002		
79	11	1.0495		1855	DILAGYGAGVA	135			
79	11			279	DLCGSVFL	136			
86	12	939.11		279	DLCGSVFLV	137	0.0007		
79	11			1657	DLEVTST	138			
86	12	1.0490		1657	DLEVTSTW	139	0.0002		
86	12			1657	DLEVTSTWWL	140			
86	13			2617	DLGVRVCEKM	141			
93	13			2617	DLGVRVCEKMA	142			
79	11			132	DLMGYIPL	143			
79	11	1013.1002		132	DLMGYIPLV	144	0.0630	0.0009	0.0490
79	11			132	DLMGYIPLVGA	145			
79	11			2412	DLSDGSWST	146			
79	11	1.0499		2412	DLSDGSWSTV	147	0.0008		
79	11			1883	DLVNLPA	148			
79	11			1883	DLVNLPAI	149	0.0001		
79	11	14.0052		1883	DLVNLPAIL	150	0.0001		
79	11	1.0891		2772	DLVVICESA	151			
79	11	24.0074		1134	DLYLVTRHA	152	0.0001		
86	12			1134	DLYLVTRHADV	153			
86	12			321	DMMMNWSPT	154			
86	12			1339	DQAEATAGA	155			
86	12			1339	DQAEATAGARL	156			
86	12			1339	DQAEATAGARLV	157			
86	12			994	DTAACGDI	158			
86	12			994	DTAACGDII	159			
86	12			124	DTLTCGFA	160			
86	12			124	DTLTCGFADL	161			
86	12			124	DTLTCGFADLM	162			
86	12			2673	DTRCFDST	163			
93	13								

Conservancy	Freq.	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
93	13			2673	DTRCFDSTV	164			
93	13			2673	DTRCFDSTVT	165			
86	12	1174.01		21	DVKFPGGGQI	166	0.0001		
86	12			21	DVKFPGGGQV	167			
79	11			750	EAALENLV	168			
100	14			2794	EAMTRYSA	169			
86	12			2237	EANLLWROEM	170			
93	13			1377	EIPFYGKA	171			
93	13	1174.07		1377	EIPFYGKAI	172	0.0001		
100	14	1.0506		2814	ELITSCSSNV	173	0.0002		
79	11			666	ELSPLLST	174			
79	11			666	ELSPLLSTT	175			
86	12	1174.11		2245	EMGNIIRV	176	0.0003		
86	12			1731	EQFKQKAL	177			
86	12			1731	EQFKOKALGL	178			
86	12			1731	EQFKOKALGLL	179			
86	12			1342	ETAGARLV	180			
86	12			1342	ETAGARLVW	181			
86	12			1342	ETAGARLVWL	182			
86	12			1342	ETAGARLVWLA	183			
86	12			1207	ETMRSPV	184			
86	12			1207	ETMRSPVFT	185			
86	12			1659	EWSTWV	186			
86	12	1.0132		1659	EWSTWVL	187	0.0001		
86	12	1.0491		1659	EVTSTWLV	188	0.0004		
93	13			130	FADLMGYI	189			
79	11			130	FADLMGYIPL	190			
79	11			130	FADLMGYIPLV	191			
100	14			1927	FASRGNHV	192			
86	12			1927	FASRGNHVSPT	193			
100	14			1773	FISGIQYL	194			
100	14	40.0082		1773	FISGIQYLA	195	0.1000		
100	14			1773	FISGIYLAGL	196			
79	11			1304	FLDGGCSGGA	197			
86	12	1.0818		177	FLALLSCL	198	0.0046		
86	12			177	FLALLSCLT	199			
93	13	1090.18		728	FLLADARV	200	0.2800	0.0480	0.0670
86	12			1228	FQVAHLHA	201			
86	12			1228	FQVAHLHAPT	202			
79	11			2646	FOYSPGQV	203			
100	14			2792	FTEAMTRYSA	204			
93	13			1567	FTGLTHIDA	205			



Conservancy	Freq.	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
93	13			512	FTPSPVV	206			
93	13			512	FTPSPVVG	207			
93	13			512	FTPSPVVGTT	208			
79	11			684	FTTLPALST	209			
79	11			684	FTTLPALSTGL	210			
79	11			146	GAARALAHGV	211			
86	12			992	GADTAACGDI	212			
86	12			992	GADTAACGDII	213			
86	12			1861	GAGVAGAL	214			
86	12			1861	GAGVAGALV	215			
86	12			1861	GAGVAGALVA	216			
86	12			350	GAHWGVLA	217			
79	11			1895	GALVGVV	218			
79	11			1895	GALVGVVCA	219			
79	11			1895	GALVGVVCAA	220			
86	12			1345	GARLVLA	221			
79	11			1345	GARLVVLT	222			
79	11			1345	GARLVVLATA	223			
79	11			1345	GARLVVLATAT	224			
100	14	24.0061		1916	GAVQWMNRL	225	0.0001		
100	14			1916	GAVQWMNRLI	226			
100	14			1916	GAVQWMNRLIA	227			
100	14			1333	GIGTVLDOA	228			
100	14			1333	GIGTVLDOAET	229			
100	14			1776	GIQYLAGL	230			
100	14			1776	GIQYLAGLST	231			
100	14			1776	GIQYLAGLSTL	232			
79	11			1425	GLDVSVIPT	233			
93	13	1.0126		1552	GLPVCQOHL	234	0.0001		
79	11			968	GLRDLAVA	235			
79	11	1.0114		968	GLRDLAVAV	236	0.0034		
100	14			1782	GLSTLPGNPA	237			
79	11			1782	GLSTLPGNPAL	238			
93	13	1.0488		1569	GLTHIDAHFL	239	0.0007		
93	13			28	GQVGGVYL	240			
93	13			28	GQVGGVYLL	241			
79	11			2063	GTFPINAYT	242			
79	11			2063	GTFPINAYTT	243			
100	14			1335	GTVLDQAET	244			
100	14			1335	GTVLDQAETA	245			
86	12			1863	GVAGALVA	246			
79	11			1081	GVCWTYYHGA	247			

Conservancy	Freq.	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
86	12			1670	GVLAALAA	248			
86	12			1670	GVLAALAAAYCL	249			
79	11	1.0099		161	GVNYATGNL	250	0.0001		
86	12			45	GVRATRKT	251			
100	14			2619	GVRVCEKM	252			
100	14			2619	GVRVCEKMA	253			
100	14	1.0504		2619	GVRVCEKMAL	254	0.0002		
93	13	1.0095		154	GVRVLEDGV	255	0.0001		
79	11			1900	GVVCAAIL	256			
100	14			1234	HAPTGSGKST	257			
100	14			1572	HIDAHLSQT	258			
86	12	939.14	*	696	HLHQIVDV	259	0.0100	0.0014	0.5400
79	11			1719	HLPIEQGM	260			
93	13	1174.08	*	1769	HMWNFISGI	261	0.3300	0.0004	0.1300
79	11			698	HQIVDVQYL	262			
79	11			222	HTPGCVPCV	263			
86	12			2855	HTPVNSWL	264			
86	12			2855	HTPVNSWLGNI	265			
79	11			1910	HVGPGEA	266			
79	11			1910	HVGPGEAV	267			
86	12			1933	HVSPTHYV	268			
100	14			1925	IAFASRGNHV	269			
79	11	1073.06	*	1856	ILAGYGAGV	270	0.0430	0.0300	2.0000
79	11	40.0140		1856	ILAGYGAGVA	271	0.0002		
86	12			1816	ILGGWVAA	272			
86	12	1090.16	*	1816	ILGGWVAAQL	273	0.0430	0.0024	0.0190
86	12			1816	ILGGWVAAQLA	274			
86	12			1331	ILGIGTVL	275			
86	12			1331	ILGIGTVLDQA	276			
93	13			1891	ILSPGALV	277			
93	13	24.0065	*	1891	ILSPGALV	278	0.0210	0.0004	0.3700
93	13			1891	ILSPGALVW	279			
79	11	1.0500		2591	IMAKNEVFCV	280	0.0088		
100	14			1777	IQYLAGLST	281			
100	14			1777	IQYLAGLSTL	282			
86	12			2250	ITRVESENKV	283			
86	12			2250	ITRVESENKV	284			
100	14			2816	ITSCSSNV	285			
100	14			2816	ITSCSSNVSV	286			
100	14			2816	ITSCSSNVSV	287			
86	12			989	ITWGADTA	288			
86	12			989	ITWGADTAA	289			

Conservancy	Freq.	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
79	11			1296	ITYSTYKFL	290			
79	11			1296	ITYSTYKFLA	291			
79	11			2613	IVFDLGV	292			
79	11	1.0503		2613	IVFDLGV RV	293	0.0016		
93	13			30	IVGGVLL	294			
86	12			1736	KALGLLOT	295			
86	12			1736	KALGLLQTA	296			
86	12			2625	KMALYDVV	297			
86	12			1734	KOKALGLL	298			
86	12			1734	KOKALGLLOT	299			
86	12			1734	KOKALGLLQTA	300			
86	12			121	KVIDTLTCGFA	301			
86	12			1255	KVLNPSV	302	0.0048		
100	14	1174.05		1255	KVLNPSVA	303			
100	14			1255	KVLNPSVAA	304			
100	14			1244	KVPAAYAA	305			
79	11	24.0068		1672	LAALAAAYCL	306	0.0011		
86	12			1305	LADGGCSGA	307			
79	11			1729	LAEOFKKA	308			
86	12			1729	LAEOFKOKAL	309			
86	12			1857	LAGYGAGV	310			
79	11			1857	LAGYGAGVA	311			
79	11			1857	LAGYGAGVAGA	312			
100	14			151	LAHGVRL	313			
86	12			179	LALLSCLT	314			
79	11			972	LAVAVEPV	315			
100	14			1924	LIAFASRGNHV	316			
100	14	1.0147		2815	LITSCSSNV	317	0.0004		
100	14			2815	LITSCSSNVSV	318			
79	11	1.0826		2612	LIVFDLGV	319	0.0002		
79	11			2612	LIVFDLGV RV	320			
86	12			178	LLALLSCL	321			
86	12			178	LLALLSCLT	322			
100	14	24.0071	*	726	LLFLLADA	323	0.0230	0.0150	0.0220
93	13	1073.05	*	726	LLFLLADARV	324			
86	12			1812	LLFNILGGWV	325	1.2000	0.0380	3.1000
86	12			1812	LLFNILGGWVA	326			
93	13			729	LLADARV	327			
93	13	24.0102		1887	LLPAILSPGA	328	0.0061		
93	13			1887	LLPAILSPGAL	329			
93	13	24.0066		36	LLPRGPRL	330	0.0025		
93	13			36	LLPRGPRLGV	331			

Conservancy	Freq	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
86	12			2240	LLWRQEMGGNI	332			
93	13			1629	LLYRLGAV	333			
79	11			133	LMGYIPLV	334			
79	11			133	LMGYIPLVGA	335			
86	12			2761	LODCTMLV	336			
86	12			126	LTCGFADL	337			
86	12			126	LTCGFADLM	338			
100	14			2180	LTDP SHIT	339			
100	14			2180	LTDP SHITA	340			
86	12			1052	LTGRDKQV	341			
93	13			1570	LTHIDAHFL	342			
93	13			2176	LTSM LTDP SHI	343			
79	11			2738	LTSCGNT	344			
79	11			2738	LTSCGNTL	345			
79	11			2738	LTSCGNTLT	346			
86	12			1591	LVAYQATV	347			
86	12	40.0133		1591	LVAYQATVCA	348	0.0002		
79	11	40.0139		1853	LVDILAGYGA	349	-0.0001		
86	12			1667	LVGGVLA	350			
86	12	1.0133		1667	LVGGVLAAL	351	0.0003		
86	12			1667	LVGGVLAALA	352			
86	12			1667	LVGGVLAALAA	353			
100	14			1257	LVLNPSVA	354			
100	14			1257	LVLNPSVAA	355			
100	14			1257	LVLNPSVAAT	356			
100	14			1257	LVLNPSVAATL	357			
79	11			1884	LVNLLPAI	358			
79	11	1.0825		1884	LVNLLPAIL	359	0.0002		
86	12			1137	LVTRHADV	360			
79	11	14.0048		1137	LVTRHADVI	361	0.0001		
79	11			1137	LVTRHADVIPV	362			
79	11			1897	LVVGWCA	363			
79	11			1897	LVVGWVCAA	364			
79	11	40.0141		1897	LVVGWVCAAI	365	0.0011		
79	11			1897	LVVGWVCAAIL	366			
79	11			2773	LVVICA	367			
86	12			1348	LVVLATAT	368			
86	12	24.0069		2592	MAKNEVFCV	369	0.0022		
100	14			2179	MLTDP SHI	370			
100	14	24.0062		2179	MLTDP SHIT	371	0.0002		
100	14			2179	MLTDP SHITA	372			
93	13			322	MMMNWSPT	373			

Conservancy	Freq.	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
93	13			1418	NAVAYYRGL	374			
93	13			1418	NAVAYYRGLDV	375			
86	12			2068	NAYTTGPCT	376			
86	12			1815	NILGGWVA	377			
86	12			1815	NILGGWAA	378			
86	12			1815	NILGGWAAQL	379			
93	13			1282	NIRTVRT	380			
79	11	1174.06		1282	NIRTVRTI	381	0.0001		
79	11			1282	NIRTVRTIT	382			
79	11			1282	NIRTVRTITT	383			
86	12			2249	NITRVESENKV	384			
86	12			700	NIVDVQYL	385			
86	12			118	NLGKVIDT	386			
86	12			118	NLGKVIDTL	387			
86	12	939.18		118	NLGKVIDTLT	388	0.0006		
93	13			1886	NLLPAILSPGA	389			
86	12			2239	NLLWRQEM	390			
93	13	1174.02	*	168	NLPGCSFSI	391	0.0041		
93	13			168	NLPGCSFSIFL	392			
86	12			1460	NTCVTQTV	393			
93	13			416	NTNGSWHI	394			
86	12			14	NTNRRPODV	395			
93	13			1889	PAILSPGA	396			
93	13			1889	PAILSPGAL	397			
86	12			1889	PAILSPGALV	398			
86	12			1889	PAILSPGALVV	399			
86	12			688	PALSTGLI	400			
86	12			688	PALSTGLIHL	401			
79	11			2609	PARLIVFPDL	402			
79	11			2066	PINAYTTGPCT	403			
79	11			1295	PITYSTYGKFL	404			
93	13			2403	PLEGEGDPDL	405			
79	11	1.0093		143	PLGGAARA	406	0.0001		
79	11			143	PLGGAARAL	407			
79	11			143	PLGGAARALA	408			
93	13			1628	PLLYRLGA	409			
93	13	1.0130		1628	PLLYRLGAV	410	0.0001		
79	11			2667	PMGFSYDT	411			
79	11			2807	POPEYDLEL	412			
79	11			2807	POPEYDLELI	413			
79	11			2807	POPEYDLELIT	414			
93	13			7	PORKTKRNT	415			

Conservancy	Freq	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
86	12			109	PTDPRRRSRNL	416			
79	11			1473	PTFTIETT	417			
79	11			1473	PTFTIETT	418			
100	14			1236	PTSGGKST	419			
93	13			1236	PTSGGKSTKV	420			
86	12			1936	PTHVPESDA	421			
86	12			1936	PTHVPESDAA	422			
79	11			1621	PTLHGPTPL	423			
79	11			1621	PTLHGPTPL	424			
79	11			2870	PTLWARM	425			
79	11			2870	PTLWARMIL	426			
79	11			2870	PTLWARMILM	427			
79	11			2870	PTLWARMILMT	428			
100	14			1626	PTPLLYRL	429			
93	13			1626	PTPLLYRLGA	430			
93	13			1626	PTPLLYRLGAV	431			
100	14	1174.13		2857	PVNSWLGNI	432	0.0001		
100	14	1174.14		2857	PVNSWLGNIH	433	0.0001		
86	12			2857	PVNSWLGNIIM	434			
79	11			2318	PVHGCPL	435			
93	13	1.0471		508	PVYCFTSPV	436	0.0004		
93	13			508	PVYCFTSPVV	437			
86	12			1340	QAETAGARL	438			
86	12			1340	QAETAGARLV	439			
86	12			1340	QAETAGARLVV	440			
86	12			1603	QAPPSWDQM	441			
93	13			1595	QATVCARA	442			
79	11			1595	QATVCARAQA	443			
93	13			29	QVGGVYL	444			
93	13	1.0088		29	QVGGVYLL	445	0.0015		
86	12			336	QLLRIPQA	446			
86	12	1.0497		2164	QLPCEPEPDV	447	0.0002		
79	11			2210	QLSAPSLKA	448			
79	11			2210	QLSAPSLKAT	449			
86	12			1465	QTVDFSLDPT	450			
86	12			1229	QVAHLHAPT	451			
86	12			1186	RAAVCTRGV	452			
79	11			1186	RAAVCTRGVA	453			
100	14	24.0063		149	RALAHGVRV	454	0.0001		
100	14			149	RALAHGVRVL	455			
86	12			2733	RASGVLTT	456			
79	11			43	RLGVRATRKT	457			

Conservancy	Freq	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
79	11	1090.21	.	2918	RLHGLSAFSL	458	0.0280	0.0055	0.0160
79	11			2611	RLVFPDL	459			
79	11	1090.22	.	2611	RLVFPDLGV	460	0.0890	0.0110	1.0000
79	11			1618	RLKPTLHGPT	461			
86	12			1029	RLAPITA	462			
86	12			1347	RLVVLATA	463			
86	12			1347	RLVVLATAT	464			
100	14			619	RLWHYPCT	465			
86	12			317	RMAWDMM	466			
93	13			635	RMVVGVEHRL	467			
86	12			2243	ROEMGGNI	468			
86	12			2243	ROEMGGNIT	469			
86	12			2243	ROEMGGNITRV	470			
79	11			1284	RTGVRTIT	471			
79	11			1284	RTGVRTITT	472			
100	14			2621	RVCEKMAL	473			
86	12			2621	RVCEKMALYDV	474			
86	12			2252	RVESENK	475	0.0001		
86	12	1.0138		2252	RVESENKV	476			
79	11			2100	RVGDRHV	477			
86	12			156	RVLEDGVNYA	478			
86	12			156	RVLEDGVNYAT	479			
86	12			2833	RVVYLTRDPT	480			
79	11			1655	SADLEVVT	481			
79	11			1655	SADLEVVTST	482			
79	11			2212	SAPSLKAT	483			
79	11			2212	SAPSLKATCT	484			
93	13			2207	SASOLSAPSL	485			
100	14			175	SIFLLALL	486			
86	12			175	SIFLLALLSCL	487			
100	14			1470	SLDPTFTI	488			
86	12			1470	SLDPTFTIET	489			
79	11			1470	SLDPTFTIETT	490			
79	11	1174.15		2926	SLHSYSPGEI	491	0.0008		
86	12	1.0478		1051	SLTGRDNQV	492	0.0002		
100	14	1174.10		2178	SMLTDPHSI	493	0.0053		
100	14			2178	SMLTDPHSIT	494			
100	14			2178	SMLTDPSHITA	495			
86	12			2163	SQLPCEPEPDV	496			
93	13			2209	SQLSAPSL	497			
79	11			2209	SQLSAPSLKA	498			
79	11			2209	SQLSAPSLKAT	499			

Conservancy	Freq.	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
93	13			56	SQPRGRROPI	500			
86	12			1242	STKVPAAYA	501			
79	11			1242	STKVPAAYAA	502			
100	14			1784	STLPGNPA	503			
79	11	40.0083		1784	STLPGNPAI	504	0.0007		
79	11			2	STNPKPQPKT	505			
86	12			1663	STWLVGGV	506			
86	12			1663	STWLVGGVL	507			
86	12			1663	STWLVGGVLA	508			
86	12			1299	STYGKFLA	509			
100	14			1262	SVAATLGFGA	510			
86	12	1.0124		1455	SVIDCNTCV	511	0.0088		
86	12			1455	SVIDCNTCVT	512			
86	12			995	TAACGDII	513			
86	12			1343	TAGARLVV	514			
86	12			1343	TAGARLVVL	515			
86	12			1343	TAGARLVVLA	516			
79	11			1343	TAGARLVLAT	517			
79	11			2852	TARHTPVNSWL	518			
79	11			2590	TIMAKNEV	519			
93	13			1266	TLGFGAYM	520			
86	12			1266	TLGFGAYMSKA	521			
79	11			1622	TLHGPTPL	522	0.0070		
79	11	1.0129		1622	TLHGPTPLL	523			
86	12			1811	TLLFNILGGW	524			
79	11	1.0108		686	TLPALSTGL	525	0.0003		
79	11	1174.03		686	TLPALSTGLI	526	0.0004		
79	11			1785	TLPGNPAI	527			
86	12	1.0092		125	TLTCGFADL	528	0.0003		
86	12			125	TLTCGFADLM	529			
79	11			2871	TLWARMIL	530			
79	11			2871	TLWARMILM	531			
79	11			2871	TLWARMILMT	532			
86	12			1209	TMRSVPFT	533			
86	12			1464	TQTVDFSL	534			
86	12			1464	TQTVDFSLDPT	535			
79	11			2589	TTIMAKNEV	536			
79	11			685	TTLPALST	537			
79	11			685	TTLPALSTGL	538			
79	11			685	TTLPALSTGLI	539			
86	12			1208	TTMRSPVFT	540			
79	11			2739	TTSCGNL	541			



Conservancy	Freq.	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
79	11			2739	TTSCGNLT	542			
79	11			1597	TVCARAQA	543			
86	12			1466	TVDFSLDPT	544			
86	12			1466	TVDFSLDPTFT	545			
100	14			1336	TVLDOAET	546			
100	14			1336	TVLDOAETA	547			
86	12			1336	TVLDOAETAGA	548			
100	14			1263	VAAATLGFGA	549			
93	13			1263	VAAATLGFGAYM	550			
86	12			1230	VAHLHAPT	551			
86	12			1440	VATDALMT	552			
86	12	40.0071		1592	VAYOATVCA	553	0.0005		
79	11			1592	VAYOATVCAR	554			
100	14	24.0064		1420	VAYYRGLDV	555	0.0001		
100	14			1420	VAYYRGLDVSV	556			
86	12			1456	VIDCNTCV	557			
86	12			1456	VIDCNTCVT	558			
86	12			1456	VIDCNTCVTQT	559			
86	12			122	VIDTLTCGFA	560			
86	12	1090.20		1671	VLAALAAAYCL	561	0.0500	0.0087	0.0047
93	13			1521	VLCECYDA	562			
79	11			1521	VLCECYDAGCA	563			
100	14			1337	VLDQAETA	564			
86	12			1337	VLDQAETAGA	565			
86	12			157	VLEDGVNYA	566			
86	12			157	VLEDGVNYAT	567			
100	14			1258	VLNPSVAA	568			
100	14			1258	VLNPSVAAT	569			
100	14	1.0483		1258	VLNPSVAATL	570	0.0015		
79	11			2737	VLTTSCGNT	571			
79	11	1.0505		2737	VLTTSCGNLT	572	0.0002		
79	11			2737	VLTTSCGNLT	573			
79	11			1852	VLVDILAGYGA	574			
86	12			1666	VLVGGVLA	575			
86	12	24.0075		1666	VLVGGVLAA	576	0.0270	0.0130	0.3100
86	12	1.0492		1666	VLVGGVLAAL	577	0.0084		
86	12			1666	VLVGGVLAALA	578			
100	14			1256	VLVLNPSV	579			
100	14	24.0072		1256	VLVLNPSVA	580	0.0009		
100	14			1256	VLVLNPSVAA	581			
100	14			1256	VLVLNPSVAAT	582			
79	11			2600	VOPEKGRKPA	583			

# HCV A02 Super Motif With Binding Information

Conservancy	Freq.	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
100	14			1918	VQWMNRLI	584			
100	14			1918	VQWMNRLIA	585			
100	14			1918	VQWMNRLIAFA	586			
86	12			1463	VTQTVDFSL	587			
79	11			1138	VTRHADVI	588			
79	11			1138	VTRHADVIPV	589			
86	12			1661	VTSTWVLV	590			
86	12			1661	VTSTWLVGGV	591			
79	11			1439	VVATDALM	592			
79	11			1439	VVATDALMT	593			
79	11			1901	VVCAAILRRHV	594			
79	11			1898	WGVVCAA	595			
79	11			1898	WGVVCAA	596			
79	11			1898	WGVVCAAIL	597			
86	12			1660	VTSTWVL	598			
86	12	1.0823		1660	VTSTWVLV	599	0.0003		
86	12	24.0070		1766	WAKHMWNFI	600	0.0001		
86	12			76	WAQPGYPWPL	601			
86	12			2873	WARMILMT	602			
79	11			2297	WARPDPNPPL	603			
100	14	24.0073		1920	WMNRLIAFA	604	0.0410	0.0330	3.0000
79	11			557	WMNSTGFT	605			
86	12			1665	WLVGGVL	606			
86	12	40.0075		1665	WLVGGVLA	607	0.0005		
86	12	40.0135		1665	WLVGGVLA	608	0.0015		
86	12			1665	WLVGGVLAAL	609			
79	11			1249	YAAQGYKV	610			
79	11			1249	YAAQGYKVL	611			
79	11			1249	YAAQGYKVLV	612			
79	11			1249	YAAQGYKVLVL	613			
79	11	1.0817		136	YPLVGAPL	614	0.0050		
100	14			1779	YLAGLSTL	615			
86	12	1.0479		1165	YKGGSSGGPL	616	0.0002		
86	12			1165	YKGGSSGGPLL	617			
93	13	1073.07		35	YLLPRRGPRL	618	0.0400	0.0007	0.0220
79	11			2836	YLTRDPTT	619			
86	12			1590	YLVAYQAT	620			
86	12	1013.02		1590	YLVAYQATV	621	0.2500	0.1100	0.6300
86	12			1590	YLVAYQATVCA	622			
86	12	1.0119		1136	YLVTRHADV	623	0.0110	0.0021	2.8000
79	11			1136	YLVTRHADVI	624			
93	13			1594	YQATVCARA	625			

Conservancy	Freq	Peptide	Filed	Position	Sequence	SeqID Num	A*0201	A*0202	A*0203
79	11			1594	YQATVCARAQ	626			
79	11			1106	YTNVDQDL	627			
79	11			1106	YTNVDQDLV	628			
86	12	1.0100		276	YWGDLGGSV	629	0.0018		
86	12			276	YWGDLGGSVFL	630			
93	13	1.0107		637	YVGGVEHRL	631	0.0008		
86	12			1939	YVPESDAA	632			
86	12			1939	YVPESDAAA	633			
86	12			1939	YVPESDAAARV	634			

Table IX  
HCV A03 Super Motif (With Binding Information)

Conservancy	Freq	Position	Sequence	SeqId Num	Filed	Peptide	A*0301	A*1101	A*3101	A*3301	A*6801
86	12	647	AACHWTRGER	635	.	24 0103	0 0003	0 0140	0 0450	0 0055	0 0018
79	11	147	AARALAHGVR	636	.						
79	11	1187	AAVCTIRGVAK	637	.						
79	11	2208	ASQLSAPSLK	638	.						
86	12	1265	ATLFGAYMSK	639	.						
79	11	48	ATRKTSER	640	.						
79	11	1188	AVCTRGVAK	641	.	1090 23	0 0260	0 0250	0 0011	0 0004	0 0001
86	12	2941	CLRKLGVPPLR	642	.						
79	11	555	CTWMNSTGFTK	643	.	3 0438	0 7600	0 7500			
79	11	2599	CVOPEKGGR	644	.	1 0961	0 0008	0 0005			
79	11	2599	CVOPEKGGPK	645	.	1 0501	0 0011	0 0008			
100	14	1574	DAHFLSOTK	646	.	24 0076	0 0003	0 0005			
93	13	2617	DLGVRVCEK	647	.	1 0144	0 0003	0 0002	0 0006	0 0440	0 0002
79	11	1143	DVIPVRRR	648	.						
86	12	2245	EMSGNITH	649	.						
86	12	2596	FVFCVQPEK	650	.	1090 24	0 0008	0 0270	0 0003	0 0005	0 4500
100	14	728	FLLADAR	651	.						
79	11	146	GAARALAHGVR	652	.						
100	14	1916	GAVQWMNR	653	.						
79	11	3037	GYLLPNR	654	.						
79	11	1004	GLPVSARR	655	.						
86	12	1131	GSSDLVLTIR	656	.						
86	12	1863	GVAGALVAFK	657	.	1073 10	0 3900	1 4000	0 0055	0 0011	0 0680
79	11	3035	GVGYLLPNR	658	.	1090 25	0 0014	0 0140	0 1500	0 0130	0 0007
79	11	45	GVRATRTKTSER	659	.						
79	11	1900	GVVCAAILR	660	.						
79	11	1900	GVVCAAILRR	661	.						
93	13	33	GYLLPRR	662	.						
93	13	33	GYLLPRRGPR	663	.						
79	11	1141	HADVIPR	664	.						
79	11	1141	HADVIPVR	665	.						
79	11	1141	HADVIPVRRR	666	.						
100	14	1234	HAPTSKGSK	667	.						
93	13	1234	HAPTSKGSKTK	668	.						
100	14	1572	HIDAHFLSOTK	669	.						
86	12	1232	HI HAPTSKGSK	670	.	1073 16	0 5900	0 0024	0 0005	0 0006	0 0028
100	14	1395	HLIFCHSK	671	.						
100	14	1395	HLIFCHSKK	672	.	1090 26	0 0250	0 0006	0 0003	0 0004	0 0010
100	14	1395	HLIFCHSKKK	673	.	1073 12	0 0260	0 0002	0 0009	0 0006	0 0001
79	11	2928	HSYSPGEINR	674	.						
79	11	222	HTPGCVPCVR	675	.	1 1061	0 0004	0 0012			
86	12	2250	ITRVESENK	676	.	1 0137	0 0150	0 0079	0 0007	0 0006	0 0092
86	12	1296	ITYSTYK	677	.						
79	11	2613	IVFPNLGVR	678	.	1 0962	0 0036	0 0044			
93	13	30	IVGGVYLLPR	679	.	1 1060	0 0008	0 0056			
93	13	30	IVGGVYLLPRR	680	.						
86	12	2944	KLGVPPLR	681	.						
86	12	10	KTKRNTNR	682	.						
86	12	10	KTKRNTNRR	683	.						
93	13	51	KTSERSQPR	684	.	24 0085	0 0110	0 0100			
86	12	51	KTSERSQPRR	685	.	1 0952	0 1600	0 0640	0 2700	0 0160	0 0550
96	12	1729	LAEOFKOK	686	.						

Conservancy	Freq	Position	Sequence	SeqID Num	Filed	Peptide	A*0301	A*1101	A*3101	A*3301	A*6801
86	12	2235	LIEANLLWR	687		1 0959	0 0008	0 0005	0 0018	0 0069	0 0008
100	14	1396	LIFCHSKK	688							
100	14	1396	LIFCHSKKK	689		1 0123	0 5400	0 1900	0 0071	0 0012	0 0240
79	11	2612	LVFPDLGVR	690		1 1066	0 0003	0 0001			
100	14	726	LLFLLADAR	691		1090 28					
93	13	36	LLPRRGPR	692							
86	12	97	LLSPRGSR	693							
79	11	1591	LVAYQATVCAR	694							
79	11	1	MSINPKPOR	695							
79	11	1	MSINPKPQPK	696							
86	12	2249	NITRVESEIK	697		1 0498	0 0010	0 0062			
79	11	14	NINRRPOOVK	698		2 0168	0 0010	0 0007			
79	11	1295	PITYSTYCK	699							
79	11	2667	PMGFSYDTR	700							
93	13	514	PSVWVGTTDR	701							
79	11	1607	PSWDXMMWK	702							
86	12	109	PTDPRRRSR	703		1 0954	0 0008	0 0005			
93	13	1236	PTGSGKSTK	704		1 0121	0 0002	0 0001	0 0006	0 0006	0 0002
93	13	516	PWVGTTDR	705		1 0956	0 0008	0 0005			
86	12	1340	QAEATAGAR	706							
93	13	29	QIVGGVLLPR	707							
86	12	289	QLFTFSPR	708							
79	11	289	QLFTFSPR	709		1 0955	0 7500	0 0330	0 0290	0 0077	3 1000
79	11	2210	QLSAPSLK	710							
79	11	1186	RAAVCTRGVAK	711							
100	14	149	RALAHGVR	712							
79	11	47	RATRKTSER	713							
79	11	43	RLGVRATR	714							
79	11	43	RLGVRATRK	715		1073 11	0 9400	0 0290	0 0420	0 0004	0 0001
100	14	1923	RLIAFASR	716							
79	11	2611	RLVFPDLGVR	717							
100	14	635	RMVVGGEHR	718		1073 13	0 7200	0 0200	0 1900	0 0030	0 0045
93	13	55	RSQPRGRR	719							
79	11	2207	SASLSAPSLK	720							
86	12	1132	SSDLYLVTR	721							
79	11	2	STNPKPOR	722		24 0089	0 0003	0 0044			
79	11	2	STNPKPQPK	723							
79	11	2	STNPKPQRTK	724							
86	12	1266	TLGFGAYMSK	725		1073 14	0 0810	0 0610	0 0005	0 0013	0 0009
79	11	1622	TUHGPTLLYR	726							
93	13	52	TSESRQPR	727							
86	12	52	TSESRQPRGR	728		24 0107	0 0003	0 0001			
86	12	52	TSESRQPRGR	729							
86	12	1050	TSLTGRDK	730							
86	12	1864	VAGALVAFK	731		24 0000	0 2400	0 8900	0 0048	0 0025	0 0310
79	11	1592	VAYQATVCAR	732		1 1064	0 0005	0 0038	0 0680	0 0720	0 0280
86	12	1337	VLDQAEATAGAR	733							
79	11	1138	VTRHADVIPVR	734							
79	11	1901	VVCAAILR	735							
79	11	1901	VVCAAILR	736							
79	11	1898	VVGWCAAILR	737							
93	13	517	VWVGTTDR	738							

Conservancy	Freq	Position	Sequence	SeqID Num	Filed	Peptide	A*0301	A*1101	A*3101	A*3301	A*6801
86	12	93	WAGWLLSPR	739							
86	12	96	WLLSPRGSR	740		1 0953	0 0008	0 0005			
100	14	1920	WMNRLLAFASR	741							
79	11	557	WMNSTGFTK	742		1174 16	0 0530	0 0810	0 0014	0 0420	0 0056
93	13	35	YLLPRRGPR	743		1 0951	0 0054	0 0005			
79	11	2930	YSPGEINR	744							
100	14	637	YGGVEIR	745							
86	12	1939	YVPESDAAR	746		1 1065	0 0003	0 0001			

Table X

HCV A24 Super Motif with Binding Information

Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401
ALLSPGAI	747	1890		8	13	93	
ALALGVRVI	748	150	1013 16	9	14	100	
ALSTGRIIL	749	689	1013 12	9	12	86	
ALVVGVRGAAI	750	1896		11	11	79	
ALFNLPGGSE	751	165		10	13	93	
ALLGFGAY	752	1265		8	14	100	
ALLGFGAYM	753	1265		9	13	93	
AVATYRGI	754	1419		8	14	100	
AVQWNRRI	755	1917		8	14	100	
AVQWNRRI	756	1917	1174 09	9	14	100	
AVQWNRRIAF	757	1917		11	14	100	
AWIMMNRW	758	319		8	12	86	
ATAAGLTKVI	759	1248		10	11	79	0 0009
ATYRLIVSVI	760	1421		11	14	100	
CLPKICVPEL	761	2941	1 0510	10	12	86	
CLWMMILL	762	739		8	12	86	
CLCGSSDI	763	1128		8	11	79	
CLCGSSDIY	764	1128	1669 62	9	11	79	
CLCGSSDIYL	765	1128		10	11	79	
CLRWVAKAVDF	766	1190		11	11	79	
CLWMSIGCF	767	555		9	11	79	
CVTOIVDF	768	1462		8	12	86	
CVTOIVDFSL	769	1462	1 0487	10	12	86	
CYDAAGCAW	770	1525		8	11	79	
CYDAAGCAW	771	1525	1 0125	9	11	79	
CYDAAGCAWTEL	772	1525		11	11	79	
DFSLDPTF	773	1468		8	14	100	
DFSLDPTF	774	1468		10	14	100	
DLCGSVEL	775	279		8	12	86	
DLEWTSTW	776	1657		9	12	86	
DLEVVISTWVL	777	1657		11	12	86	
DLGVRVCEKM	778	2617		10	13	93	
DLMGVPL	779	132		8	11	79	
DLVNLPLAI	780	1883	14 0052	9	11	79	
DLVNLPLAIL	781	1883	1 0891	10	11	79	
DLAAGGDI	782	994		8	12	86	
DLAAGGDI	783	994		9	12	86	
DLTCGFADL	784	124		10	12	86	
DLTCGFADLM	785	124		11	12	86	
DLKFAKGGKA	786	21	1174 01	10	12	86	
DYFTRWVG	787	615		9	14	100	
EIPFYGKAI	788	1377		9	13	93	
ETAGARLVVL	789	1342	1174 07	10	12	86	
ETIMRSFVF	790	1207		9	12	86	
EVVTSIWWL	791	1659	1 0132	9	12	86	

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency (%)	Conservancy (%)	A*2401
FISGQYI	792	773		8	14	100	
FISGQPLAGI	793	773		11	14	100	
FILALISCI	794	777	1 0818	9	12	86	
FILAMIV	795	792		8	14	100	
FICLTHIDAF	796	767		11	13	93	
FILPAISICL	797	684		11	11	79	
FWAKRWNF	798	765	24 0092	9	12	86	6 9000
FWAKRWNF	799	765		10	12	86	
GFALIMGY	800	729		8	13	93	
GFALIMGY	801	729		9	13	93	
GFALIMGYPL	802	729		11	11	79	
GFSTIIRF	803	769		9	11	79	
GDYLAIR	804	776		8	14	100	
GDYLAISIL	805	776		11	14	100	
GFVIGIR	806	752	1 0126	9	13	93	
GFVIGIR	807	752		11	12	86	
GSFISHSY	808	7921	1073 03	10	11	79	0 0001
RLSTLPNPAL	809	782		11	11	79	
GLTHIDAF	810	769		9	13	93	
GLTHIDAF	811	769	1 0488	10	13	93	
STFPYAY	812	7063		8	11	79	
GVAGALVAF	813	783		9	12	86	
GVAKAVDF	814	793		8	11	79	
GVLAALAA	815	7670	1174 19	9	12	86	
GVLAALAAAYCL	816	7670		11	12	86	
GVNATGNL	817	761	1 0099	9	11	79	
GVNCEKM	818	7619		8	14	100	
GVNCEKMA	819	7619	1 0504	10	14	100	
GVNCEKMAIY	820	7619		11	14	100	
GVNCEKMAIY	821	754		11	12	86	
GVVCAAI	822	7900		8	11	79	
GVVCAAI	823	7900		8	11	79	
GVVCAAI	824	7900		11	11	79	
GVVCAAI	825	7900	13 0133	10	12	86	0 0003
GVVCAAI	826	7900	13 0131	10	11	79	0 0057
GVVCAAI	827	7900		11	12	86	
GVVCAAI	828	7900		11	11	79	
GVVCAAI	829	7900		9	11	79	
GVVCAAI	830	7900	1174 08	9	13	93	
GVVCAAI	831	7900		11	13	93	
GVVCAAI	832	7900		8	12	86	
GVVCAAI	833	7900		11	12	86	
GVVCAAI	834	7900		11	11	79	
GVVCAAI	835	7900		10	12	86	
GVVCAAI	836	7900	1090 16	10	12	86	0 0026



Sequence	SeqId Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401
ILGLTIVL	837	1331		8	12	86	
IMAKREVI	838	2591		8	12	86	
ITSTIGKE	839	1296		9	12	86	
ITSTIGKEI	840	1296		10	11	79	
IVWDYLY	841	701		8	12	86	
IVGVYLI	842	30		8	13	93	
KPSFAA	843	23		8	13	93	
KVDTITCF	844	121		10	12	86	
IFNIGFW	845	1813		8	12	86	
IEADLW	846	2235		8	12	86	
IQINRSW	847	414		8	11	79	
ILALSL	848	178		8	12	86	
ILAPLAY	849	1030		8	14	100	
ILFNLGFW	850	1812		9	12	86	
ILFALSPGAL	851	1887		11	13	93	
ILPRRGR	852	36	24 0066	9	13	93	
ILSPRRSRPSW	853	97		11	11	79	
ILWRKMAFNI	854	2240		11	12	86	
ITCGAL	855	126		8	12	86	
ITCGALIM	856	126		9	12	86	
ITCGALRMGY	857	126		11	12	86	
ITHDHF	858	1570		8	13	93	
ITHDHFI	859	1570		9	13	93	
ITSMITDPSHI	860	2176		11	13	93	
ITTCGNI	861	2738		9	11	79	
LVDRAGY	862	1853		8	11	79	
LVGVLAAL	863	1667	1 0133	9	12	86	
LVINPSVAATL	864	1257		11	14	100	
LVNLPAL	865	1884		8	11	79	
LVNLPAL	866	1884	1 0825	9	11	79	
LVTRHADI	867	1137	14 0948	9	11	79	
LVGVVCAAL	868	1897	40 0141	10	11	79	
LVGVVCAAL	869	1897		11	11	79	
LWARMIM	870	2872		8	12	86	
LWARMIMTHF	871	2872		11	12	86	
LWARMIMTHF	872	2241		10	12	86	
LWARMIMTHF	873	1135		11	11	79	
MLMTHFF	874	2876		8	12	86	
MLTDFSHI	875	2179		8	14	100	
MWNPISGL	876	1770		8	14	100	
MWNPISGL	877	1770		10	14	100	
MWNPISGL	878	1770		11	14	100	
MWNPISGL	879	636	1073 18	10	13	93	0 0270
MYGAVNIFRL	880	1772		8	14	100	
NFISGL	881	1772	24 0091	9	14	100	0 0170
NFISGL							

Sequence	SeqID#	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401
RLICAWVAAGI	882	1815		11	12	86	
RLRICARRD	883	1282	1174 06	9	11	79	
RLMIVGPH	884	700		8	12	86	
RLMIVGPIY	885	700	1073 01	9	12	86	0.0001
RLCKVDFI	886	318	939 18	9	12	86	
RLIWRJEM	887	2239		8	12	86	
RLPGVSGI	888	168	1174 02	9	13	93	
RLPGVSGP	889	168		10	13	93	
RLPGVSGPI	890	168		11	13	93	
RLVLIQVIF	891	1460		10	12	86	
RLNGSWH	892	316		8	13	93	
RLNGSWK	893	14		11	11	79	
RLNGSWW	894	1108		9	11	79	
RLNGSWW	895	551		8	12	86	
RLTSGYGI	896	1295		10	11	79	
RLTSGYGI	897	1295		11	11	79	
RLTSGYGI	898	2403		11	13	93	
RLTSGYGI	899	143	1 0093	9	11	79	
RLTSGYGI	900	2667		11	11	79	
RLTSGYGI	901	109		11	12	86	
RLTSGYGI	902	1621		9	11	79	
RLTSGYGI	903	1621		10	11	79	
RLTSGYGI	904	1621		11	11	79	
RLTSGYGI	905	2870		8	11	79	
RLTSGYGI	906	2870		9	11	79	
RLTSGYGI	907	2870		10	11	79	
RLTSGYGI	908	1626		8	14	100	
RLTSGYGI	909	1554		9	12	86	
RLTSGYGI	910	1554		10	12	86	
RLTSGYGI	911	2857	1174 13	9	14	100	
RLTSGYGI	912	2857	1174 14	10	14	100	
RLTSGYGI	913	2857		11	12	86	
RLTSGYGI	914	2318		8	11	79	
RLTSGYGI	915	1732		9	12	86	
RLTSGYGI	916	1732		10	12	86	
RLTSGYGI	917	29		8	13	93	
RLTSGYGI	918	29	1 0088	9	13	93	
RLTSGYGI	919	1465		11	12	86	
RLTSGYGI	920	1919		9	14	100	
RLTSGYGI	921	1778	13 0075	9	14	100	0.0480
RLTSGYGI	922	2647	13 0134	10	11	79	0.0180
RLTSGYGI	923	2647		11	11	79	
RLTSGYGI	924	2918		8	12	86	
RLTSGYGI	925	2918	1090 21	10	11	79	0.0001
RLTSGYGI	926	2611		8	11	79	

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A:2401
RLAPLAY	927	1029	1174 18	9	12	86	
RMADMMMM	928	317		8	12	86	
RMADMMNNW	929	317		10	12	86	
RMIMMTHF	930	2875		8	12	86	
RMIMMTHF	931	2875		9	12	86	
RMVAVVHRL	932	635		11	13	93	
RVEIKMAL	933	2621		8	14	100	
RVEIKMAL Y	934	2621	1174 21	9	14	100	
RVEIKMAY	935	156	1174 17	9	12	86	
SFSEILAI	936	173		9	14	100	
SFSEILAI I	937	173	24 0108	10	14	100	0 0041
SFSEILAI I	938	175		8	14	100	
SFSEILAI SGI	939	175		11	12	86	
SLDPTFI	940	1470		8	14	100	
SLHSVPR I	941	2926	1174 15	10	11	79	
SMIDPSHI	942	2178	1174 10	9	14	100	
SKVPAA Y	943	1242		8	12	86	
SILPGNPAI	944	1784	40 0083	9	11	79	
STWLVGMI	945	1663		10	12	86	
SVAATIGF	946	1262		8	14	100	
SVAATIGFAY	947	1262		11	14	100	
SWCKMMWGI	948	1608		9	11	79	
SWLGNIM	949	2860		8	12	86	
SYKGSAGPI	950	1164		11	12	86	
TIMAKNEVF	951	2590		9	11	79	
TIGFGAYM	952	1266		8	13	93	
TIHGPTFI	953	1622		8	11	79	
TIHGPTFI L	954	1622	1 0129	9	11	79	
TIHGPTFI Y	955	1622	1073 04	10	11	79	0 0001
TLFNILGGW	956	1811		10	12	86	
TLPAI STGL	957	686		9	11	79	
TLPALSTGI I	958	686	1 0108	10	11	79	
TLPGNPAI	959	1785	1174 03	8	11	79	
TLTCGFADL	960	125	1 0092	9	12	86	
TLTCGFADIM	961	125		10	12	86	
TLWARMII	962	2871		8	11	79	
TLWARMIL M	963	2871		9	11	79	
TLIMAKNEVF	964	2589		10	11	79	
TLIPAL STGL	965	685		10	11	79	
TLIPALSTGI I	966	685		11	11	79	
TIMPSPVF	967	1208		8	12	86	
TTSCGNIL	968	2739		8	11	79	
TVDPSIDPTF	969	1466		10	12	86	
TWMNSTGI	970	556		8	11	79	
TWLVGSL	971	1664		9	12	86	

# ICV A24 Super Motif With Binding Information

Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*1401
LVSLVGR	972	1297	13 0074	8	13	93	0.0240
LVSLVGR1	973	1297		9	12	86	
VSLVGR1	974	1566		8	13	93	
VSLVGR1	975	1272	109020	9	12	86	0.0070
VLAAALAA	976	1671		8	12	86	
VLAAALAA1	977	1671		10	12	86	
VLAAALAA1	978	157	1 0483	8	12	86	0.0070
VLAAALAA1	979	1258		10	14	100	
VLAAALAA1	980	2737		10	11	79	
VLAAALAA1	981	1852	1 0492	9	11	79	0.0016
VLAAALAA1	982	1666		10	12	86	
VLAAALAA1	983	2639		8	11	79	
VLAAALAA1	984	1463	107319	10	11	79	0.0016
VLAAALAA1	985	1138		8	12	86	
VLAAALAA1	986	1439		8	11	79	
VLAAALAA1	987	1898	1 0817	9	11	79	0.0001
VLAAALAA1	988	1898		10	12	86	
VLAAALAA1	989	1660		8	13	93	
VLAAALAA1	990	34	1 0479	11	14	100	0.0001
VLAAALAA1	991	1920		8	12	86	
VLAAALAA1	992	1665		11	12	86	
VLAAALAA1	993	136	107307	9	11	79	0.0001
VLAAALAA1	994	1779		8	14	100	
VLAAALAA1	995	1165		10	12	86	
VLAAALAA1	996	35	1 0107	10	13	93	0.0001
VLAAALAA1	997	1136		8	11	79	
VLAAALAA1	998	1106		11	11	79	
VLAAALAA1	999	276	1 0107	10	12	86	0.0001
VLAAALAA1	1000	637		9	13	93	
VLAAALAA1	1001	1422		10	14	100	
VLAAALAA1	1002						
VLAAALAA1	1003						
VLAAALAA1	1004						
VLAAALAA1	1005						
VLAAALAA1	1006						

Table Xi  
ICV B07 Super Motif (with Binding Information)

Conservancy	Freq	Position	Sequence	SeqID Num	Filed	Peptide	R*5702	R*3501	R*5101	R*5301	R*5401
86	12	1604	APPSWDOM	1007		15 0051	0 002R	0 0002	0 0002	0 0001	0 0002
79	11	1604	APPSWDOMW	1008		15 0233	0 0001	0 0001	0 0002	0 0006	0 0003
93	13	1235	APTSGSKTKV	1009		29 0117	0 0001				
79	11	2869	APTLWARM	1010	*	29 0031	0 4300	0 0031	0 0012	0 0002	0 0023
79	11	2869	APTLWARM	1011	*	15 0063	0 0160	0 0002	0 0012	0 0001	0 0002
79	11	2869	APTLWARMIL	1012	*	15 0247	0 8800	0 0001	0 0010	0 0001	0 0003
79	11	2869	APTLWARMILM	1013	*	29 0118	0 0130	0 0001	0 0003	0 0002	0 0033
79	11	2410	DPDLSGSW	1014		15 0058	0 0001	0 0002	0 0002	0 0005	0 0002
86	12	111	DPRRSRNL	1015	*	15 0043	0 0170	0 0002	0 0001	0 0001	0 0002
79	11	2615	FDLGVVR	1016		29 0032	0 0001	0 0002			
100	14	24	FPGGGV	1017		29 0033	0 0001				
100	14	24	FPGGGVGV	1018		29 0119	0 0001				
86	12	1912	GPFGAVOW	1019		15 0055	0 0001	0 0032	0 0002	0 0001	0 0002
86	12	1912	GPFGAVOWM	1020		15 0240	0 0001	0 0031	0 0002	0 0001	0 0003
93	13	41	GPRLGVRA	1021		29 0034	0 0001				
100	14	1625	GPTPLLYRL	1022		15 0053	0 0024	0 0032	0 0002	0 0001	0 0002
93	13	1625	GPTPLLYRLGA	1023		29 0120	0 0005				
93	13	507	GPVCFTPSPV	1024		29 0121	0 0001				
93	13	1378	IPFYGKAI	1025	*	29 0035	0 0120	0 0031	0 1200	0 0002	0 2000
79	11	137	IPLVGAPL	1026	*	29 0036	0 4400	0 0032	0 0700	0 0003	0 0035
86	12	2608	KPARLIVF	1027	*	29 0037	0 0150	0 0032	0 0017	0 0002	0 0006
79	11	2608	KPARLIVFPDL	1028		29 0122	0 0003				
79	11	1620	KPTLHGPTPL	1029	*	15 0234	1 4150	0 0031	0 0002	0 0001	0 0003
79	11	1620	KPTLHGPTPL	1030		29 0123	0 0021				
93	13	1888	LPAILSPGA	1031	*	16 0013	0 0001	0 0001	0 0001	0 0002	0 9400
93	13	1888	LPAILSPGAL	1032	*	15 0238	0 0053	0 0001	0 0036	0 0001	0 2100
86	12	1888	LPAILSPGALV	1033		29 0124	0 0003				
100	14	687	LPALSTGL	1034	*	29 0038	0 0020	0 0002			
86	12	687	LPALSTGLI	1035		15 0048	0 0350	0 0002	2 0000	0 0062	0 0005
86	12	687	LPALSTGLIHL	1036		29 0125	0 0011				
86	12	2165	LPCEPEPDV	1037		15 0056	0 0001	0 0002	0 0001	0 0001	0 0002
93	13	169	LPGCSFSI	1038	*	29 0039	0 0110	0 0360	0 0059	0 0150	0 0016
93	13	169	LPGCSFSIF	1039	*	1145 12	0 1950	0 0796	0 0550	0 0813	0 0015
93	13	169	LPGCSFSIFL	1040	*	15 0220	0 0022	0 0009	0 0100	0 0140	0 0012
93	13	169	LPGCSFSIFLL	1041		29 0126	0 0007				
93	13	37	LPRRGPRL	1042	*	29 0040	6 5000	0 0001	0 0180	-0 0002	0 0020
93	13	37	LPRRGPRLGV	1043	*	15 0218	0 1900	0 0001	0 0009	0 0001	0 0025
93	13	1553	LPVCOOHL	1044	*	29 0041	0 0005	0 0046	0 0002	0 0110	0 0003
86	12	1553	LPVCOOHLF	1045	*	15 0232	0 0001				
86	12	1553	LPVCOOHLFW	1046	*	29 0127	0 0001				
86	12	1720	LPVCOOHLFW	1047	*	29 0042	0 0130	0 0001	0 0040	-0 0002	0 0013
100	14	1260	NPSVAATL	1048		29 0043	0 0011				
86	12	1260	NPSVAATLGF	1049		15 0230	0 0001	0 0001	0 0002	0 0001	0 0003
86	12	1605	PPPSWDOM	1050		29 0044	0 0003				
79	11	1605	PPPSWDOMW	1051		15 0052	0 0001	0 0002	0 0001	0 0001	0 0002
79	11	1606	PPSWDOMW	1052		29 0045	0 0001				
79	11	1606	PPSWDOMWKC	1053		29 0128	0 0001				
79	11	2317	PPVHGCPL	1054	*	1292 17	0 0140	0 0001	0 0001	0 0001	-0 0002
79	11	2601	QPEKGGKPA	1055	*	16 0188	0 0011	0 0001	0 0001	0 0002	0 0190
79	11	2808	QPEYOLEL	1056		29 0046	0 0002				
79	11	2808	QPEYOLEL	1057		15 0062	0 0001	0 0002	0 0002	0 0001	0 0002
86	12	78	QPGYPAWPL	1058		29 0047	0 0006				

Conservancy	Freq	Position	Sequence	SeqID Num	Filed	Peptide	B*0702	R*3501	R*5101	R*5301	R*5401
86	12	78	QPGYPMPLY	1059		15 0040	0.0001	0.0011	0.0002	0.0001	0.0002
93	13	57	QPRGRROP	1060	.	15 0039	0.2300	0.0002	0.0001	0.0001	0.0002
79	11	2299	RPDYNPPL	1061		29 0048	0.0050				
93	13	1893	SPGALVGV	1062	.	15 0054	0.0001	0.0002	0.0002	0.1200	0.0002
79	11	1893	SPGALVGV	1063	.	15 0239	0.0130	0.0001	0.0016	0.0001	0.0003
79	11	2931	SPGEINRV	1064		29 0049	0.0007				
79	11	2931	SPGEINRV	1065		16 0015	0.0003	0.0001	0.0001	0.0002	0.0037
79	11	2649	SPGORVEF	1066		29 0050	0.0027				
79	11	2649	SPGORVEFL	1067	.	15 0060	0.1200	0.0002	0.0002	0.0001	0.0002
79	11	99	SPRGRPSW	1068	.	15 0042	0.3800	0.0002	0.0005	0.0001	0.0002
86	12	1935	SPTHYVPESDA	1069		29 0129	0.0001				
86	12	1975	TPCGSWL	1070		29 0051	0.0028				
79	11	1126	TPCTCGSSDL	1071		15 0228	0.0005	0.0001	0.0002	0.0001	0.0003
79	11	1126	TPCTCGSSDLY	1072		29 0130	0.0001				
86	12	223	TPGCVPCV	1073		29 0052	0.0001				
93	13	1550	TPGLPVODHL	1074		29 0131	0.0001				
93	13	1627	TPILYRLGA	1075	.	16 0017	0.0083	0.0001	0.0001	0.0002	0.2300
93	13	1627	TPILYRLGAV	1076	.	15 0235	0.0120	0.0001	0.0008	0.0001	0.0110
86	12	2856	TPVNSWLGNI	1077		15 0246	0.0001	0.0001	0.0053	0.0006	0.0003
86	12	2856	TPVNSWLGNI	1078		29 0132	0.0001				
86	12	1940	VPESDAAA	1079		29 0053	0.0022				
86	12	1940	VPESDAAARV	1080		15 0241	0.0001	0.0001	0.0010	0.0001	0.0003
86	12	799	WPLLLLLL	1081		29 0054	0.0021				
100	14	616	YPYRLWHY	1082		29 0055	0.0001				

Table XII

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Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)
AKHWNFI	1083	1767		8	12	86
AKIEVFCV	1084	2593		8	12	86
AFALAHGV	1085	148		8	14	100
DIEELSP	1086	663		8	11	79
EKGGRKA	1087	2603		8	11	79
EKMALYDV	1088	2624		8	12	86
FKCKALCL	1089	1733		8	12	86
GHRMAWDM	1090	315		8	13	93
GKSTKVA	1091	1240		8	12	86
GKPARLI	1092	2606		8	11	79
HRMAWDM	1093	316		8	13	93
IKGGRIL	1094	1390		8	11	79
IHTGVRTI	1095	1283		8	11	79
KKCDELA	1096	1403		8	14	100
KKCDELA	1097	1402		8	14	100
LIIGPTLL	1098	1623		8	11	79
IKKIVDV	1099	697		8	12	86
LIHLAVAV	1100	969		8	11	79
RIIVSPHY	1101	1932		8	12	86
PIGGRKA	1102	58		8	13	93
PIGGRSW	1103	100		8	11	79
PIHRSRL	1104	112		8	12	86
RIADVIP	1105	1140		8	11	79
RIIPVNSW	1106	2854		8	12	86
RKLGVPPL	1107	2943		8	12	86
HKPARLIV	1108	2607		8	11	79
RRCRASGV	1109	2730		8	13	93
RIKGRILGV	1110	39		8	13	93
RRPQVKE	1111	17		8	12	86
SKKFCDEL	1112	1401		8	14	100
SRILGKVI	1113	116		8	12	86
THIDAHFL	1114	1571		8	13	93
TKIKLTI	1115	2985		8	12	86
TKVPAAYA	1116	1243		8	12	86
IRKFDSTV	1117	2674		8	14	100
IRGVAKAV	1118	1191		8	11	79
VHVCLKMA	1119	2620		8	14	100
VHMEDGV	1120	155		8	13	93
YIRLDVSV	1121	1423		8	14	100
ARRIIPVNSW	1122	2853		9	11	79
ARIIVFPDL	1123	2610		9	11	79
ARLVVLAIA	1124	1346		9	11	79
ARMILMTHF	1125	2874		9	12	86
ARPIYNPPL	1126	2298		9	11	79
DRSELSPL	1127	663		9	11	79

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
EKMAIYIVV	1128	2624		9	12	86
EKGJALGLI	1129	1733		9	12	86
GHRMAWIMMM	1130	315		9	13	93
GKSTKVPAA	1131	1240		9	12	86
GRRPARIV	1132	2606		9	11	79
HRMAWIMMM	1133	316		9	12	86
IKGGRHIF	1134	1390		9	11	79
KKCLIFLAA	1135	1402		9	14	100
LHGLSAGSL	1136	2919		9	11	79
LHGPIILY	1137	1623		9	11	79
LHSYSGRI	1138	2927		9	11	79
LKSSSGPI	1139	1166		9	12	86
LKRLVAFPI	1140	2942		9	12	86
NIASFTHVV	1141	1932		9	12	86
PRRKLWKE	1142	16		9	11	79
PRRRPRCV	1143	38		9	13	93
RRHPVNSWL	1144	2854		9	12	86
RRMPCFCA	1145	1909		9	11	79
RKPARIVF	1146	2607		9	11	79
RGRBASGL	1147	2730		9	12	86
RHSRLGKV	1148	114		9	12	86
SRKRCIEIA	1149	1401		9	14	100
THYVFSQA	1150	1937		9	12	86
TKVPAAYAA	1151	1243		9	11	79
TRHADVPV	1152	1139		9	11	79
THVSGNKV	1153	2251		9	12	86
VRPFGQJ	1154	22		9	13	93
VIVCEKML	1155	2620		9	14	100
WRLLAPITA	1156	1028		9	11	79
WRKMLQJH	1157	2242		9	12	86
YRGLDVSVI	1158	1423		9	14	100
YRRGRASGV	1159	2729		9	13	93
ARALAHGVIV	1160	148		10	14	100
ARAQAPPSW	1161	1600		10	11	79
ADHHPVNSWL	1162	2853		10	11	79
AHMLMTHF	1163	2874		10	12	86
CHSKKCTEL	1164	1399		10	14	100
DRLRSLSPL	1165	661		10	11	79
DRCETSPIL	1166	663		10	11	79
EKGJRPAR	1167	2603		10	11	79
FRAAVCTRCV	1168	1185		10	12	86
GHRMAWIMMM	1169	315		10	12	86
GKSTKVPAAV	1170	1240	24 0036	10	12	86
GRRPARIVF	1171	2606		10	11	79
KHAWRIISHI	1172	1768		10	13	93



Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)
KKCTETLAARK	1173	1403		10	12	86
LEKQIMVDY	1174	697		10	11	79
LEKQVAFPL	1175	1166		10	12	86
QKALALQTA	1176	1735		10	12	86
RRVAFACAV	1177	1909		10	11	79
RRVAFACAV	1178	39		10	13	93
RRVAFACAV	1179	1908		10	11	79
RRVAFACAV	1180	113		10	12	86
RRVAFACAV	1181	114		10	12	86
SKGGYAKDV	1182	2552		10	12	86
SKKKLHIAA	1183	1401		10	14	100
THVVEALAA	1184	1937		10	12	86
THVAKAVDF	1185	1191		10	11	79
THVSEKAV	1186	2251		10	12	86
VKLYAFZAV	1187	22		10	13	93
VHVEKMAFY	1188	2620		10	14	100
VHVEFWNY	1189	155		10	12	86
WHLEAPLAY	1190	1028		10	11	79
YKLVIRFSV	1191	1254		10	14	100
YHREKASGL	1192	2729		10	12	86
AKGVHVEIKGV	1193	152		11	13	93
AKHMMHESGI	1194	1767		11	12	86
ARALALGVRL	1195	148		11	14	100
ARLVIRFGV	1196	2610		11	11	79
CHSKKLELA	1197	1399		11	14	100
DRGRSLPIL	1198	661		11	11	79
EKGGRPARL	1199	2603		11	11	79
FRAAVCTRGVA	1200	1185		11	11	79
GKSTRVFAAYA	1201	1240		11	12	86
GKVIDHLAGF	1202	120		11	12	86
HMMAMMMNNW	1203	316		11	12	86
KKCTETLAARK	1204	1402		11	12	86
KRNINHPQDV	1205	12		11	12	86
LHGPTPLVRL	1206	1623		11	11	79
LKQNMVQDL	1207	697		11	11	79
LKPTLHGPPL	1208	1619		11	11	79
LEHVAFFEGA	1209	1907		11	11	79
PERGFACVRA	1210	38		11	13	93
PERSEPLGKV	1211	112		11	12	86
RRVAFACAV	1212	1908		11	11	79
RRSSNLGKI	1213	113		11	12	86
SRGRIVSPHY	1214	1929		11	12	86
SRNLGRVDTL	1215	116		11	12	86
THVPELQAAA	1216	1937		11	12	86
VHVEKNNVA	1217	155		11	12	86

Sequence	Caspl(3) Dom	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
YKVI VLP <sup>2</sup> NA	1218	1253		11	14	100

Table XIII

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Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)
AAILRHIV	1219	1904		8	13	93
AAL AAYCL	1220	1673		8	12	86
AACXKVL	1221	1250		8	11	79
AAILGFGA	1222			8	14	100
AAVCTRGV	1223	1187		8	12	86
ASIMAFIA	1224	1793		8	11	79
ASSASOL	1225	2204		8	14	100
ATLGFGAY	1226	1265		8	14	100
CSFSIFLL	1227	172		8	14	100
CSGGAYDI	1228	1310		8	12	86
CSNVSVVA	1229	2819		8	14	100
CICGSSQL	1230	1128		8	11	79
CIRGVAKA	1231	1190		8	11	79
DTAACGDI	1232	934		8	12	86
DILTCGFA	1233	124		8	12	86
EALENLV	1234	750		8	11	79
EAMIRYSA	1235	2794		8	14	100
ESDAARV	1236	1942		8	12	86
ETAGARLV	1237	1342		8	12	86
ETIMRSPV	1238	1207		8	12	86
FADLMGYI	1239	130		8	13	93
FASIQNHV	1240	1927		8	14	100
FSIFLLAL	1241	174		8	14	100
FSYDTRCF	1242	2670		8	11	79
FTEAMTRY	1243	2792		8	14	100
FIPSPWV	1244	512		8	13	93
GAGVAGAL	1245	1861		8	12	86
GAHWGVLA	1246	350		8	12	86
GALWGWV	1247	1895		8	11	79
GARLVLA	1248	1345		8	12	86
GSGKSTKV	1249	1238		8	13	93
GSSDLVLY	1250	1131		8	12	86
GSSCGPRL	1251	1168		8	12	86
GSSYGFOY	1252	2641		8	11	79
GTFPINAY	1253	2063		8	11	79
HSYSFGEI	1254	2928		8	11	79
HIIPNSWL	1255	2855		8	12	86
ISGIOYLA	1256	1774		8	14	100
ITSCSSNV	1257	2816		8	14	100
IHWGADTA	1258	989		8	12	86
KSTKVPAA	1259	1241		8	12	86
LAGYGAGV	1260	1857		8	11	79
LAHGRVL	1261	151		8	14	100
LAVAVEPV	1262	972		8	11	79
LSAPSLKA	1263	2211		8	11	79

Sequence	SeqS Match	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
LSPTAVV	1264	1892		8	13	93
LSQAHH	1265	690		8	12	86
LTCTFAH	1266	126		8	12	86
LTEDAH	1267	1570		8	13	93
MSAHEVV	1268	1654		8	11	79
FWHCFH	1269	2859		8	14	100
NICVIV	1270	1460		8	12	86
NINFWH	1271	416		8	13	93
PAISFA	1272	1889		8	13	93
PAISTGH	1273	688		8	12	86
PLWARM	1274	2870		8	11	79
PEPLVH	1275	1626		8	14	100
QAVVAGA	1276	1595		8	13	93
RABRWFM	1277	3019		8	14	100
RSELSH	1278	664		8	11	79
RSEHGRV	1279	115		8	12	86
SASFHSH	1280	2923		8	11	79
SSASQISA	1281	2206		8	14	100
STKVPAAV	1282	1242		8	12	86
STLPRFA	1283	1784		8	14	100
STLFQVM	1284	2633		8	12	86
STYKHA	1285	1299		8	12	86
TAACTH	1286	995		8	12	86
TAGARLV	1287	1343		8	12	86
TIMSPVF	1288	1208		8	12	86
TISGTH	1289	2739		8	11	79
VAGAVAF	1290	1864		8	12	86
VTHADVI	1291	1138		8	11	79
VTSIWWLV	1292	1661		8	12	86
WAKIMWF	1293	1766		8	12	86
WAKVIVM	1294	368		8	14	100
WADVGFV	1295	76		8	12	86
YAAQVTKV	1296	1249		8	11	79
YSIFPLH	1297	2905		8	11	79
YSTGKFI	1298	1298		8	12	86
YTHVXHL	1299	1106		8	11	79
AAKLQJLTM	1300	2758		9	16	114
AAQYKVLV	1301	1250		9	11	79
AARAHGV	1302	147		9	11	79
AATLGFAY	1303	1264		9	14	100
AAVCIRVA	1304	1187		9	11	79
ASQISAFSL	1305	2208		9	13	93
ATLFGAYM	1306	1265		9	26	186
ATVCAAOA	1307	1596		9	11	79
CAAHFRHV	1308	1903		9	13	93

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
CAWVELTPA	1309	1530		9	11	79
CSFSEFLA	1310	172		9	14	100
CSFAYEHL	1311	1310		9	12	86
CHGSSJLY	1312	1128	1 0118	9	11	79
CHGVAKAV	1313	1190		9	11	79
CIWNNSIGF	1314	555		9	11	79
DACCAWVEL	1315	1527		9	11	79
DTAACGDI	1316	994		9	12	86
DHGETLSIV	1317	2673		9	13	93
ETAGARLVV	1318	1342		9	12	86
FTIMRSPVF	1319	1207		9	12	86
FSFLLALL	1320	174		9	14	100
FSLDPTFL	1321	1469		9	14	100
FTGLTHEDA	1322	1567		9	13	93
GAGVAGALV	1323	1861		9	12	86
GALVAIKIM	1324	1866		9	12	86
GALVAIKVM	1325	1866		9	14	100
GAVDMMRIL	1326	1916	24 0061	9	14	100
HSPKPDDEL	1327	1400		9	14	100
HIFGVPCV	1328	222		9	11	79
ITWGAUTAA	1329	989		9	12	86
ITVSTGRKF	1330	1296		9	12	86
KALGLIOTA	1331	1736		9	12	86
KSTKVPAAV	1332	1241	13 0016	9	12	86
LAALAAATCL	1333	1672	24 0068	9	12	86
LAEOFKOKA	1334	1729		9	12	86
LAGLAYYSM	1335	356		9	14	100
LAGYGAGVA	1336	1857		9	11	79
LSAFSLHSY	1337	2922		9	11	79
LSTLPGNPA	1338	1783	13 0019	9	14	100
LTCGFADLM	1339	126		9	24	171
LTDPSHITA	1340	2180		9	14	100
LTGRKQOV	1341	1052		9	12	86
LTHDAHFL	1342	1570		9	13	93
LITSCGNIL	1343	2738		9	11	79
MAPLEVFCV	1344	2532		9	12	86
MAWIMMMNW	1345	318	24 0069	9	13	93
NAVATYRGL	1346	1418		9	12	86
NSLRH#IM	1347	2481		9	14	100
NSWLGNIIM	1348	2859		9	24	171
NINFRPCOV	1349	14		9	12	86
PAILSPGAI	1350	1889		9	13	93
PSVAATLGF	1351	1261		9	14	100
PTLHGPTPL	1352	1621		9	11	79
PTLWARMIL	1353	2870		9	11	79

Sequence	SeqIDNum	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
OAE LAIARL	1354	1340		9	12	86
RAAVLIRGV	1355	1386		9	12	86
RAIAIRVRV	1356	149	24 0063	9	14	100
RACAFPPSW	1357	1601		9	11	79
RAYAMIRRM	1358	811		9	16	114
RSLSPILL	1359	664		9	11	79
RSPNIGKVI	1360	115		9	12	86
SSASQI SA	1361	2205		9	14	100
STKVPAAVA	1362	1242		9	12	86
STLPQNPAL	1363	1784	40 0083	9	11	79
STWLVKGV	1364	1663		9	12	86
TAGARI VVI	1365	1343		9	12	86
TSCSNVSV	1366	2817		9	14	100
TIMAKNFV	1367	2589		9	11	79
VAAIIGFA	1368	1263		9	14	100
VAGGIRVVM	1369	933		9	14	100
VATQAVCA	1370	1592	40 0071	9	12	86
VATIRGLDV	1371	1420	24 0064	9	14	100
VSIILQAVM	1372	2632		9	12	86
VTDVDFSL	1373	1463		9	12	86
WAKHWNFI	1374	1766	24 0070	9	12	86
YAGGGRVI	1375	1249		9	11	79
YAPTIWARM	1376	2868		9	14	100
YSPGFNRV	1377	2930		9	11	79
YSPGFNFF	1378	2648		9	11	79
YSTIGKLA	1379	1298		9	12	86
YTNVCKIV	1380	1106		9	11	79
YAGGGRVI VI	1381	1250		10	11	79
AATLGFAYM	1382	1264		10	26	186
ASLRVFTEAM	1383	2787		10	12	86
ASSASQI SA	1384	2204		10	14	100
ATGNLPGSF	1385	165		10	13	93
CSFSIFLLAL	1386	172		10	14	100
CIGGSSIRTL	1387	1128		10	11	79
DARVCACIWM	1388	733		10	18	129
DSMDNICY	1389	1454		10	12	86
DILTCGFAL	1390	124		10	12	86
ENILWQGM	1391	2237		10	24	171
ETAGARV VVI	1392	1342		10	12	86
FADI MGYHFI	1393	130		10	11	79
FTEAMIRYSA	1394	2792		10	14	100
GAHALARGV	1395	146		10	11	79
GADTAACGDI	1396	992		10	12	86
GAGVAGALVA	1397	1861		10	12	86
GALVVGVCAL	1398	1895		10	11	79

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
GAHVVVLAIA	1399	1345		10	11	79
GAVDMMIRLI	1400	1916		10	14	100
GSJKSTKVFA	1401	1238		10	12	86
GVLDQAEFA	1402	1335		10	14	100
HSKKKGLHIA	1403	1400		10	14	100
IAFASRGRIV	1404	1925		10	14	100
ISGIGYLAGL	1405	1774		10	14	100
IRVLSIRPKV	1406	2250		10	12	86
ITSSSNVSV	1407	2816		10	14	100
IYSTYGRFL	1408	1296		10	11	79
KSTKVFAAYA	1409	1241		10	12	86
LAHGRSGSA	1410	1305		10	11	79
LAHGRKAL	1411	1729		10	12	86
LALPHAYAM	1412	806		10	12	86
LSFGALVVGV	1413	1892		10	13	93
LSPRRSRRSW	1414	98		10	11	79
LSRAIRHWF	1415	3017		10	14	100
LSILGNPAL	1416	1783		10	11	79
LHPITKYM	1417	1642		10	16	114
NIQVIGVDF	1418	1460		10	12	86
PAISFGALV	1419	1889		10	12	86
PAISGLIHL	1420	688		10	12	86
PARIVFFPL	1421	2609		10	11	79
PSWDXMKKCL	1422	1607		10	11	79
PTGSGNSTAV	1423	1236		10	13	93
PTHVVFSDA	1424	1936		10	12	86
PTLHGPIPL	1425	1621		10	11	79
PTLWARMILM	1426	2870		10	22	157
PTPLLRIGA	1427	1626		10	13	93
QAEIAGARLV	1428	1340		10	12	86
QAPPSWDJIM	1429	1603		10	24	171
QATVCARAOA	1430	1595		10	11	79
RAAKLQDCIM	1431	2757		10	16	114
RAAVCTIRGVA	1432	1186		10	11	79
RAIAHGVRL	1433	149		10	14	100
SASQISAPSL	1434	2207		10	13	93
STKVFARAA	1435	1242		10	11	79
SIWLVGSL	1436	1663		10	12	86
TAGARLVVLA	1437	1343		10	12	86
TARHVPVSW	1438	2852		10	11	79
TSSSNVSWA	1439	2817		10	14	100
TSMILDFSHI	1440	2177		10	13	93
TSMWLVGGV	1441	1662		10	12	86
TIIMAKNEVF	1442	2589		10	11	79
TILPAISGLI	1443	685		10	11	79

Sequence	Length (Residues)	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
VAAIIIGGAAZ	1444	1263	10	14	100
VIFGIFGSGM	1445	1507	10	16	114
VIFGAIIVHVV	1446	1138	10	11	79
WAFVGVWPI	1447	76	10	12	86
WARRMIMTHF	1448	2873	10	12	86
WAFIVVHPI	1449	2297	10	11	79
YAGGGRKLV	1450	1249	10	11	79
YSGGIRHVA	1451	2930	10	11	79
YSGGIRHFI	1452	2648	10	11	79
AARALAHGVRV	1453	147	11	11	79
AAELHVEHFM	1454	2786	11	12	86
AAVETHGVAKA	1455	1187	11	11	79
ASGHPVHGM	1456	1717	11	14	100
ASQISAPSLKA	1457	2208	11	11	79
CARAGAPPSW	1458	1599	11	11	79
CSISSEILAL	1459	172	11	14	100
CICGSSILYV	1460	1128	11	11	79
CTRGVAKAVDF	1461	1190	11	11	79
DARVACIWMW	1462	733	11	16	114
DILICGALIM	1463	124	11	24	171
ETAGALVLA	1464	1342	11	12	86
FALHMGVPLV	1465	130	11	11	79
FSHSYSPGFI	1466	2925	11	11	79
FICLTHDAHF	1467	1567	11	13	93
FTILFALSTIL	1468	684	11	11	79
GAUTAACGDI	1469	992	11	12	86
GAGVAGALVAF	1470	1861	11	12	86
GALVVGVVCAA	1471	1895	11	11	79
GAVOMNRLLA	1472	1916	11	14	100
GSGRSLKVVAA	1473	1248	11	12	86
HSKPKCEIAA	1474	1400	11	14	100
HSYSPGFNRV	1475	2928	11	11	79
HIFNFGWIGF	1476	2855	11	12	86
IIRVSEFNKV	1477	2250	11	12	86
IIFGSSNVVA	1478	2816	11	14	100
IYSTYKFLA	1479	1296	11	11	79
KSTKVPAAVAA	1480	1241	11	11	79
LAKKSGGAY	1481	1305	11	11	79
LAGYGAGVAGA	1482	1857	11	11	79
LSNQLPRHNM	1483	2479	11	14	100
LSPGALVVGV	1484	1892	11	11	79
LICGADMGY	1485	126	11	12	86
LISMIDPSHI	1486	2176	11	13	93
NAVATTRGLDV	1487	1418	11	13	93
NINRPQVKE	1488	14	11	11	79



Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)
PAIISFGALVV	1489	1889		11	12	86
PSVAAILGFGA	1490	1261		11	14	100
PIIIRRRRRRI	1491	109		11	12	86
PIIPVPEGLAA	1492	1936		11	12	86
PIIIRRRRIIV	1493	1621		11	11	79
PIIPIIRRGAV	1494	1626		11	13	93
QALTAGALVV	1495	1340		11	12	86
QAPPSMWXMM	1496	1603		11	11	79
QIMIRSLPTE	1497	1465		11	12	86
RRRRRRRRRPI	1498	55		11	13	93
SALIFVVTSLW	1499	1655		11	11	79
SSASRRSAPSI	1500	2206		11	13	93
SSSIVIVIRRA	1501	1132		11	12	86
SIWLVVAVIA	1502	1663		11	12	86
TARRHPVPSWI	1503	2852		11	11	79
TSIIGRRRRIV	1504	1050		11	12	86
TSIWWVGGVI	1505	1662		11	11	79
TLIPALSLGLI	1506	685		11	12	86
VAATLGFGLYM	1507	1263		11	11	79
VAGALVAKVM	1508	1864		11	26	186
VAVIPVPSLM	1509	974		11	14	100
VAYQALVAKRA	1510	1592		11	12	86
VAYTRRLIVSV	1511	1420		11	11	79
VTSIWWLVKIV	1512	1661		11	14	100
WAQPGYKWLIV	1513	76		11	12	86
WARMILMTHF	1514	2873		11	12	86
YAAQGYKVLVI	1515	1249		11	11	79
YATGNIPGCSF	1516	164		11	12	86
YINNDKDLVGV	1517	1106		11	11	79

Table XIV

HCV B62 Super Motif

Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)
AISPGAL	1518	1890		8	13	93
ALAHGVRV	1519	150		8	14	100
ALGILQTA	1520	1737		8	12	86
APTLWARH	1521	2869	29 0031	8	11	79
AOAPPPSW	1522	1602		8	12	86
AUGYKVLV	1523	1251		8	11	79
AVAYYRGL	1524	1419		8	14	100
AVCTRQVA	1525	1188		8	11	79
AVQWMNHL	1526	1917		8	14	100
CLWMMLLI	1527	739		8	12	86
CMSADLEV	1528	1653		8	11	79
CXXHLEFW	1529	1556		8	12	86
CVTIQVDF	1530	1462		8	12	86
DHAGTGA	1531	1855		8	12	86
IXGGSVEL	1532	279		8	12	86
ELMGYIPL	1533	132		8	11	79
DLVNILPA	1534	1883		8	11	79
DJAETAGA	1535	1339		8	12	86
EIPFYGKA	1536	1377		8	13	93
EUFKQKAL	1537	1731		8	12	86
EVVTSIYW	1538	1659		8	12	86
FISQIYTL	1539	1773		8	14	100
FDKGVRRV	1540	2615	29 0032	8	11	79
FDGGLLV	1541	24	29 0033	8	14	100
FOVAHIIHA	1542	1228		8	12	86
GIQYLAL	1543	1776		8	14	100
GLRLAVA	1544	968		8	11	79
GPHLGVR	1545	41	29 0034	8	13	93
GQVIGVY	1546	28		8	14	100
GVAGALVA	1547	1863		8	12	86
GVAKAVDF	1548	1193		8	11	79
GVLAAALAA	1549	1670		8	12	86
GVRCERKM	1550	2619		8	14	100
GWCAAIL	1551	1900		8	11	79
HNGRCEGA	1552	1910		8	11	79
HVSPHIVV	1553	1933		8	12	86
ILGGWVAA	1554	1816		8	12	86
ILGIGIVL	1555	1331		8	12	86
ILSPGALV	1556	1891		8	13	93
IMAKNEVF	1557	2591		8	12	86
IPFYGKAI	1558	1378	29 0035	8	13	93
IPLVGAPL	1559	137	29 0036	8	11	79
IVDVQVLY	1560	701		8	12	86
IVFDLGV	1561	2613		8	11	79
IVGGVYLL	1562	30		8	13	93

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
KMALVIVV	1563	2625	29 0037	8	12	86
KFAHIVH	1564	2608		8	12	86
KCKALILL	1565	1734		8	12	86
KVFAAYAA	1566	1244		8	11	79
LIFAPLW	1567	2235	414	8	12	86
LRIIRVW	1568	414		8	11	79
LIALLSL	1569	178		8	12	86
LIALIAY	1570	1030		8	14	100
LILADAV	1571	729	1629	8	13	93
LVRIGAV	1572	1629		8	13	93
LMGRIIV	1573	133		8	11	79
LPAISLH	1574	687		8	14	100
IFGSLSL	1575	169	29 0038	8	13	93
IFGRFIR	1576	37	29 0039	8	13	93
IFVGRH	1577	1553	29 0040	8	13	93
IFVGRM	1578	1720	29 0041	8	12	86
IQRIMV	1579	2761	29 0042	8	12	86
IVAYQATV	1580	1591		8	12	86
IVDILGY	1581	1853		8	11	79
IVGVIAA	1582	1667		8	12	86
IVINPSVA	1583	1257	1884	8	14	100
IVNLIPI	1584	1884		8	11	79
IVIRHADV	1585	1137		8	12	86
IVGVVCA	1586	1897		8	11	79
IVVGLSA	1587	2773	2876	8	12	86
MLMIRF	1588	2876		8	12	86
MLIDPSH	1589	2179		8	14	100
MLGGWA	1590	1815		8	12	86
NVDMQYL	1591	700	2239	8	12	86
NILWRFM	1592	2239		8	14	100
NPSVAATI	1593	1260		8	11	79
FLGGAARA	1594	143		8	13	93
PLLYHIGA	1595	1628	29 0044	8	12	86
FPTSWDXM	1596	1605		8	11	79
FPNWLKMW	1597	1606		8	11	79
PVHGFPI	1598	2318		8	13	93
QVGRVYL	1599	29	29 0046	8	12	86
QILRIEJA	1600	336		8	11	79
QRYRIL	1601	2808		8	12	86
QPSYFMT	1602	78		8	12	86
RIHGSAT	1603	2918	29 0047	8	11	79
RIIVFDL	1604	2611		8	12	86
RIEAPTA	1605	1029		8	12	86
RIVLATA	1606	1347		8	12	86
RIAWQMM	1607	317		8	12	86

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
IRMLMLHF	1608	2875		8	12	86
IRDYVGFY	1609	2299	29 0048	8	11	79
IRLMFZDI	1610	2243		8	12	86
IRGLKDAI	1611	2621		8	14	100
IRVSNKV	1612	2252		8	12	86
IRGLHVV	1613	2100		8	11	79
IRLLAI	1614	175		8	14	100
IRPFI	1615	1470		8	14	100
IRRFIR	1616	2931	29 0049	8	11	79
IRLRF	1617	2649	29 0050	8	11	79
IRLSAPLI	1618	2209		8	13	93
IRVAAHGF	1619	1262		8	14	100
IRAKRFV	1620	2990		8	11	79
IRGFAYM	1621	1266		8	13	93
IRHGFPI	1622	1622		8	11	79
IRFGRFI	1623	1785		8	11	79
IRWGRMI	1624	2871		8	11	79
IRCSGWL	1625	1975	29 0051	8	12	86
IRGVFVY	1626	273	29 0052	8	12	86
IRIVDFSI	1627	1464		8	12	86
IRCAHQA	1628	1597		8	11	79
IRDNFV	1629	1456		8	12	86
IRAAAIY	1630	1671		8	12	86
IRGLYDA	1631	1521		8	13	93
IRNDALIA	1632	1337		8	14	100
IRFGVNY	1633	157		8	12	86
IRNPSVAA	1634	1258		8	14	100
IRVGVIA	1635	1666		8	12	86
IRVNFV	1636	1256		8	14	100
IRVSSYGF	1637	2639		8	11	79
IRVSDAAA	1638	1940	29 0053	8	12	86
IRVNNRIL	1639	1918		8	14	100
IRVATDALM	1640	1439		8	11	79
IRGVVCAA	1641	1898		8	11	79
IRVTSWVL	1642	1660		8	12	86
IRVNRILAI	1643	1920		8	14	100
IRVLIILL	1644	799	29 0054	8	12	86
IRVIVGVNI	1645	1665		8	12	86
IRVAGLSII	1646	1779		8	14	100
IRVIRVHGF	1647	616	29 0055	8	14	100
IRVPSDAA	1648	1939		8	12	86
IRSPGAIY	1649	1890	24 0067	9	12	86
IRAHGVRI	1650	150	1 0094	9	14	100
IRSLGRII	1651	689	1 0109	9	12	86
IRVGVVCA	1652	1896	40 0089	9	11	79

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
APFSSWIKIM	1654	1604	15 0051	9	12	86
APILWAHMI	1654	2869	15 0063	9	11	79
AGSKKIVL	1655	1551		9	11	79
AGYSIFWFL	1656	77		9	12	86
AGVMMIRLI	1657	1917	1174 09	9	14	100
CMSEALFVV	1658	1653	1 0131	9	11	79
DECSMILV	1659	279	1 0101	9	11	79
DEVVISTW	1660	1657		9	12	86
DMGYPLV	1661	132	1 0816	9	11	79
DVRLIFAI	1662	1883	14 0052	9	11	79
DVVFESA	1663	2772		9	11	79
DYLVIRIA	1664	1134	24 0074	9	12	86
DELSQSW	1665	2410	15 0058	9	11	79
DEFRSRRL	1666	111	15 0043	9	12	86
EPFYKAI	1667	1377	1174 07	9	13	93
EMKMITRV	1668	2245	1174 11	9	12	86
EVVISTWV	1669	1659	1 0132	9	12	86
FESIQYLA	1670	1773	40 0082	9	14	100
FILALSEL	1671	177	1 0818	9	12	86
FILITADRV	1672	728	1 0113	9	13	93
FQSPKRW	1673	2646		9	11	79
SGMIDXA	1674	1333		9	14	100
GLPQDRL	1675	1552	1 0126	9	13	93
GLRDAVAV	1676	968	1 0114	9	11	79
GLTHIDAR	1677	1569		9	13	93
GFTEGAVDW	1678	1912	15 0055	9	12	86
GFPLLYRI	1679	1625	15 0053	9	14	100
GAWGGVYL	1680	28		9	13	93
GAAGALVAF	1681	1863		9	12	86
GLAALAAV	1682	1670	1 0134	9	12	86
GVNATGNI	1683	161	1 0099	9	11	79
GVVCEKMA	1684	2619		9	14	100
GVVLEIXV	1685	154	1 0095	9	13	93
HHQRIIDV	1686	696	1 0111	9	12	86
HPVIEQIM	1687	1719		9	11	79
HMWIEGIL	1688	1769	1174 08	9	13	93
IRVIVVQY	1689	698		9	11	79
IRKPFCAV	1690	1910		9	11	79
IRAGYAGV	1691	1856	1 0135	9	11	79
ISPGALVV	1692	1891	24 0065	9	13	93
KVIVNFSV	1693	1255	1174 05	9	14	100
LITSCSSNV	1694	2815	1 0147	9	14	100
LIVFDLGV	1695	2612	1 0826	9	11	79
LIFILLADA	1696	726	24 0071	9	14	100
LIPNIGRW	1697	1812		9	12	86

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
LIHRRAR	1698	36	24 0066	9	13	93
IPALSPGA	1699	1888	16 0013	9	13	93
IPALSLGI	1700	687	15 0048	9	12	86
IPFIFETW	1701	2165	15 0056	9	12	86
IPFISGIF	1702	169	15 0044	9	13	93
IPFIMAAI	1703	1667	1 0133	9	12	86
LVINPSVAA	1704	1257	1 0825	9	14	100
LVNLIPIAI	1705	1884	14 0048	9	11	79
LVTHIAIV	1706	1137		9	11	79
LVVGVVCAA	1707	1897		9	11	79
NHGGWVAA	1708	1815		9	12	86
NIRIGVRII	1709	1282	1174 06	9	11	79
NVWVRIY	1710	700	1 0112	9	12	86
NIGKVIDII	1711	118	1 0091	9	12	86
NIPVCSLS	1712	168	1174 02	9	13	93
NVKKVAV	1713	1108		9	11	79
PIGGAAAI	1714	143	1 0093	9	11	79
PIIYRGA	1715	1628	1 0130	9	13	93
PPSSWIKMW	1716	1605	15 0052	9	11	79
PPVIRAFI	1717	2317	29 0070	9	11	79
PXFEYRII	1718	2807		9	11	79
PVYKRII	1719	1554		9	12	86
PVNSWIGFI	1720	2857	1174 13	9	14	100
QVKGIVII	1721	29	1 0088	9	13	93
QUSAPSIKA	1722	2210		9	11	79
QFVRII	1723	2808	15 0062	9	11	79
QKGFWEIY	1724	78	15 0040	9	12	86
QTRFRRIPI	1725	57	15 0039	9	13	93
RLAPIIAY	1726	1029	1 0116	9	12	86
RMLMTHFI	1727	2875		9	12	86
RVCIRKAIY	1728	2621	1 0145	9	14	100
RVISETKVV	1729	2252	1 0138	9	12	86
RVIDKNNY	1730	156	1 0096	9	12	86
SMITPSHI	1731	2178	1174 10	9	14	100
SPGALVVGV	1732	1893	15 0054	9	13	93
SPGRIIRVA	1733	2931	16 0015	9	11	79
SPYKRIEII	1734	2649	15 0060	9	11	79
SPKGSFISW	1735	99	15 0042	9	11	79
SVIICNTIV	1736	1455	1 0124	9	12	86
TIKAKNEVI	1737	2590		9	11	79
TIKGPINLI	1738	1622	1 0129	9	11	79
TIPIALSTGL	1739	686	1 0108	9	11	79
TIICGFAUI	1740	125	1 0092	9	12	86
TIWAKMIM	1741	2871		9	11	79
TIPIYRGA	1742	1627	16 0017	9	13	93

Sequence	SeqID Date	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
VIIDGALIA	1743	1336		9	14	100
VIETLTCGF	1744	122		9	12	86
VIETRWNYA	1745	177		9	12	86
VIETRIAGY	1746	1852		9	11	79
VIYGGALAA	1747	1666	24 0075	9	12	86
VIYIPSSVA	1748	1256	24 0072	9	14	100
VQWMNRRIA	1749	1918		9	14	100
VVGIVVCAAI	1750	1898		9	11	79
VVTSIWWIV	1751	1660	1 0823	9	12	86
WNRRIIAFA	1752	1920	24 0073	9	14	100
WLVVWGLA	1753	1665	40 0075	9	12	86
YPLVGGAPL	1754	136	1 0817	9	11	79
YLVAYQDAIV	1755	1590		9	12	86
YVTRHAIIV	1756	1136	1 0119	9	12	86
YQAIIVCARA	1757	1594		9	13	93
YVGRCCSV	1758	276	1 0100	9	12	86
YVGRVFRR	1759	637	1 0107	9	13	93
YVPESDAAA	1760	1939		9	12	86
AVSGGALVV	1761	1890	24 0101	10	12	86
AVVGVVCAA	1762	1896		10	11	79
APFSPWIXJMW	1763	1604	15 0233	10	11	79
APILWAIMIL	1764	2869	15 0247	10	11	79
AGFGVFWFTY	1765	77		10	12	86
AVAYVGLIV	1766	1419	1 0486	10	14	100
AVCTRGVAKA	1767	1188		10	11	79
AVQWMNRRIA	1768	1917		10	14	100
CLHKLIVFFL	1769	2941	1 0510	10	12	86
CVIQIVDFSL	1770	1462	1 0457	10	12	86
DILAGYGAGV	1771	1855	1 0495	10	11	79
DLEVTSIWW	1772	1657	1 0490	10	12	86
DGVRVCEKM	1773	2617		10	13	93
DLSDGSWSIV	1774	2412	1 0499	10	11	79
DLVNLIPAL	1775	1883	1 0891	10	11	79
DQAEIAGAPL	1776	1339		10	12	86
DWFKPKGKX	1777	21	1174 01	10	12	86
ELISGSSNV	1778	2814	1 0506	10	14	100
EQPKKXAL	1779	1731		10	12	86
EVVTSIWWIV	1780	1659	1 0491	10	12	86
GLSAFSLHSY	1781	2921	1 0509	10	11	79
GLSTIPGNFA	1782	1782		10	14	100
GLTHQDAIFL	1783	1569	1 0488	10	13	93
GPFGGAVQWM	1784	1912	15 0240	10	12	86
GAVGGVYLL	1785	28		10	13	93
GVCWTVYHGA	1786	1081		10	11	79
GVRVCEKMAI	1787	2619	1 0504	10	14	100

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
ELQVIMQVH	1788	696		10	11	79
ELAGYAGVA	1789	1856	40 0140	10	11	79
ELGAWAAAL	1790	1816	1 0493	10	12	86
IMAKQEVFV	1791	2591	1 0500	10	11	79
IQYLALSTH	1792	1777		10	14	100
IVFPIRGVH	1793	2613	1 0503	10	11	79
KPILHGPTEL	1794	1620	15 0234	10	11	79
KVHSHLGFL	1795	121		10	12	86
KVLVIRPSVA	1796	1255		10	14	100
LLFNILGAWV	1797	1812	1 0890	10	12	86
LLPAILSPGLA	1798	1887	24 0102	10	13	93
LMGYHVLGA	1799	133		10	11	79
LPAILSPGAL	1800	1888	15 0238	10	13	93
LPVPSLSPT	1801	169	15 0220	10	13	93
LPKRPRLGV	1802	37	15 0218	10	13	93
LPVQXKHEF	1803	1553	15 0232	10	12	86
LVAYQATVLA	1804	1591	40 0133	10	12	86
LVHLAGYCA	1805	1853	40 0139	10	11	79
LVGGMIAALA	1806	1667		10	12	86
LVGGMVCAAL	1807	1897	40 0141	10	11	79
MLTTPSHATA	1808	2179		10	14	100
NLPKESLGF	1809	168		10	13	93
NPSVAATLGF	1810	1260	15 0230	10	14	100
PIETSTYKAF	1811	1295		10	11	79
PLGGAAHALA	1812	143		10	11	79
POFLYDELL	1813	2807		10	11	79
PVCCXKHEFW	1814	1554	1174 14	10	12	86
PVNSMLGNIL	1815	2857		10	14	100
PVYCFIFSPV	1816	508	1 0471	10	13	93
QAPCEPEPDV	1817	2164	1 0497	10	12	86
QPEKGGKRA	1818	2601	16 0188	10	11	79
RLHGLSAFSL	1819	2918	1 0508	10	11	79
RLVTFPLGV	1820	2611	1 0502	10	11	79
RMWIDMMRW	1821	317		10	12	86
RLLEDGWNVA	1822	156		10	12	86
SLHSYSPGEL	1823	2926	1174 15	10	11	79
SLTGRKRW	1824	1051	1 0478	10	12	86
SPGALVVGWV	1825	1893	15 0239	10	11	79
SQLSAPSLKA	1826	2209		10	11	79
SQLPGRGRPT	1827	56		10	13	93
SVAAHGFGLA	1828	1262		10	14	100
TLHGPTPLLY	1829	1622	1 0489	10	11	79
TLFNILGAW	1830	1811		10	12	86
TLFALSGLL	1831	686	1174 03	10	11	79
TLTGFAHLM	1832	125		10	12	86



Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
TPCTGASLR	1833	1126	15 0228	10	11	79
TPFYVRCAY	1834	1627	15 0235	10	13	93
TVNFWLGFH	1835	2856	15 0246	10	12	86
TVHSLRTH	1836	1466		10	12	86
VDRITGFA	1837	132		10	12	86
VLAALAAVCL	1838	1671	1 0889	10	12	86
VLDJAEIAGA	1839	1337		10	12	86
VINPSVAAH	1840	1258	1 0483	10	14	100
VITISGRH	1841	2737	1 0505	10	11	79
VIVGVIAAL	1842	1666	1 0492	10	12	86
VVINPSVAA	1843	1256		10	14	100
VVKSSYGFY	1844	2639		10	11	79
VPESDAAAHV	1845	1940	15 0241	10	12	86
VQMMNRHAF	1846	1918		10	14	100
VGVVVCALH	1847	1898		10	11	79
WVLVGVIAA	1848	1665	40 0135	10	12	86
YKGSSTGFL	1849	1165	1 0479	10	12	86
YLLPRRGPR	1850	35	1 0469	10	13	93
YLVTRHADV	1851	1136		10	11	79
YVGRGGSVF	1852	276		10	12	86
ALVVGWCAAL	1853	1896		11	11	79
APTSIGSSTPV	1854	1235	29 0117	11	13	93
APTLWARMIM	1855	2869	29 0118	11	11	79
AOAPPSWIDIM	1856	1602		11	12	86
AVCTRGVAKAV	1857	1188		11	11	79
AVQMMNRHAF	1858	1917		11	14	100
DLAGYGAGVA	1859	1855		11	11	79
DLEVVTSTWVI	1860	1657		11	12	86
DLGVRVCEKMA	1861	2617		11	13	93
DLMGVPLVGA	1862	132		11	11	79
DLYLVTRHADV	1863	1134		11	12	86
DGAETAGAHV	1864	1339		11	12	86
DWKEFGGKQV	1865	21		11	12	86
EDPRKAGLL	1866	1731		11	12	86
FISGRVLAAL	1867	1773		11	14	100
FLAAGGSGAFJA	1868	1304		11	11	79
FGGKGVGVAV	1869	24	29 0119	11	14	100
FGYSGQRMFF	1870	2646		11	11	79
GIQVAGLSIL	1871	1776		11	14	100
GIQVQQRHFF	1872	1552		11	12	86
GLSLPGHAF	1873	1782		11	11	79
GPIPLLYRUGA	1874	1625	29 0120	11	13	93
GFVYCFHSPV	1875	507	29 0121	11	13	93
GVLAAALAAVCL	1876	1670		11	12	86
GVRCERKMAV	1877	2619		11	14	100

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)
CAVWELIDVWY	1878	154		11	12	86
HEHJWVWY	1879	696		11	11	79
HWVWVWVWY	1880	1769		11	13	93
HEHJWVWVWY	1881	698		11	11	79
HWVWVWVWY	1882	1910		11	11	79
HEHJWVWVWY	1883	1816		11	12	86
HEHJWVWVWY	1884	1331		11	12	86
HEHJWVWVWY	1885	1891		11	13	93
HEHJWVWVWY	1886	2608	29 0122	11	11	79
HEHJWVWVWY	1887	1620	29 0123	11	11	79
HEHJWVWVWY	1888	1734		11	12	86
HEHJWVWVWY	1889	124		11	12	86
HEHJWVWVWY	1890	1255		11	14	100
HEHJWVWVWY	1891	1924		11	14	100
HEHJWVWVWY	1892	2815		11	14	100
HEHJWVWVWY	1893	2612		11	11	79
HEHJWVWVWY	1894	726		11	13	93
HEHJWVWVWY	1895	1812		11	12	86
HEHJWVWVWY	1896	1887		11	13	93
HEHJWVWVWY	1897	36		11	13	93
HEHJWVWVWY	1898	97		11	11	79
HEHJWVWVWY	1899	2240		11	12	86
HEHJWVWVWY	1900	1888	29 0124	11	12	86
HEHJWVWVWY	1901	687	29 0125	11	12	86
HEHJWVWVWY	1902	169	29 0126	11	13	93
HEHJWVWVWY	1903	1553	29 0127	11	12	86
HEHJWVWVWY	1904	1667		11	12	86
HEHJWVWVWY	1905	1257		11	14	100
HEHJWVWVWY	1906	1137		11	11	79
HEHJWVWVWY	1907	1897		11	11	79
HEHJWVWVWY	1908	1815		11	12	86
HEHJWVWVWY	1909	2249		11	12	86
HEHJWVWVWY	1910	1886		11	13	93
HEHJWVWVWY	1911	168		11	13	93
HEHJWVWVWY	1912	1295		11	11	79
HEHJWVWVWY	1913	2403		11	13	93
HEHJWVWVWY	1914	2667		11	11	79
HEHJWVWVWY	1915	1606	29 0128	11	11	79
HEHJWVWVWY	1916	2857		11	12	86
HEHJWVWVWY	1917	508		11	13	93
HEHJWVWVWY	1918	635		11	13	93
HEHJWVWVWY	1919	2243		11	12	86
HEHJWVWVWY	1920	2621		11	11	79
HEHJWVWVWY	1921	175		11	12	86
HEHJWVWVWY	1922	2178		11	14	100

Sequence	SeqID Num	Position	Peptide No.	No. of Amino Acids	Sequence Frequency	Conservancy (%)
SPTHVVP SDA	1923	1935	29 0129	11	12	86
SAHVEPEFDV	1924	2163		11	12	86
SVAAHUG GAY	1926	1262		11	14	100
ILGICATMSKA	1926	1266		11	12	86
ILFNHGGWW	1927	1811		11	12	86
IFCTLGSSRLV	1928	1126	29 0130	11	11	79
IFKAPVCFHL	1929	1550	29 0131	11	13	93
IPVNSWLGRI	1930	2856	29 0132	11	12	86
IVLDQAF TAGA	1931	1336		11	12	86
VLGCHKACGA	1932	1521		11	11	79
VLVHLAGYGA	1933	1852		11	11	79
VLVGVLAAL A	1934	1666		11	12	86
VGFKGRGRPA	1935	2600		11	11	79
VGVNMRIDFA	1936	1918		11	14	100
VVCALHFRHV	1937	1901		11	11	79
WVLVGVLAAL	1938	1665		11	12	86
VLKSSGGRLL	1939	1165		11	12	86
VLVATQATVCA	1940	1590		11	12	86
YCATVCAKAGA	1941	1594		11	11	79
YVHLGGSHL	1942	276		11	12	86
YVFLSQAAAHV	1943	1939		11	12	86

Table XV  
HCV A01 Motif with Binding Information

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101
ASGCGSPY	1944	166	26 0026	8	20	100	0.0001
DRESVLSRKY	1945	737	20 0255	10	18	90	0.0680
FAAFETGCGY	1946	631	20 0254	10	19	95	
GAAPETGCGY	1947	630		11	19	95	
GRETIVLEY	1948	140		8	15	75	
GYSINFMGY	1949	579	2 0058	9	17	85	
HILWKAGILY	1950	149	1069 04	10	20	100	0.1100
KQAFTESPY	1951	653	20 0256	10	19	95	0.0001
LIDIASALY	1952	30	1069 01	9	17	85	1.2 0000
LSUVSAALY	1953	415	1090 07	10	19	95	0.0150
LTGREIVLEY	1954	137		11	15	75	
MMYRWGPSLY	1955	360	1039 01	10	17	85	0.0810
MSITILEAY	1956	103	2 0126	9	15	75	0.8500
NSVLSRKY	1957	738	2 0123	9	18	90	0.0005
PLDKGKPY	1958	124	1147 12	9	20	100	
PLDKGKPY	1959	124	1069 03	10	20	100	0.1700
PLIGRTSLY	1960	797	1090 09	9	17	85	0.2100
SASFCGSPY	1961	165		9	20	100	
SLDVSAALY	1962	416	1069 02	9	19	95	5.2000
STIDLEAY	1963	104		8	15	75	
TIGRTSLY	1964	798	26 0030	8	17	85	
WLSIDVSAALY	1965	414	26 0551	11	19	95	0.3200
WMWVWGPS	1966	359	1039 06	11	17	85	
YEALMFLY	1967	640	19 0014	8	19	95	
YSINFMGY	1968	580	26 0032	8	17	85	

Table XVI

HCV A03 Motif with Binding Information

Conservancy	Freq	Peptide	Fold	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
86	12	24 0103	.	647	10	AACNWRGER	1969	0.0003
79	11			147	10	AARALAHGVR	1970	
100	14			1264	8	AATLGFGA	1971	
100	14			1264	9	AATLGFGAY	1972	
79	11	24 0104 40 0089	.	1187	9	AAVCTRGVA	1973	0.0003
79	11			1187	10	AAVCTRGVAK	1974	
79	11			1187	11	AAVCTRGVAKA	1975	
86	12			648	9	AACNWRGER	1976	
79	11			1306	9	AUGGGLSGA	1977	
79	11			1306	10	AUGGGLSGAY	1978	
86	12			1142	8	ADVIPVRR	1979	
79	11			1142	9	ADVIPVRRR	1980	
100	14			1926	8	AFASRGNH	1981	
86	12			1865	8	AGALVAFK	1982	
86	12	24 0104 40 0089	.	1344	9	AGARLVLA	1983	0.0003
79	11			1344	11	AGAFVLVLA	1984	
100	14			1781	11	AGLSTLPGNPA	1985	
86	12			1862	9	AGVAGALVA	1986	
86	12			1862	10	AGVAGALVAF	1987	
86	12			1862	11	AGVAGALVAFK	1988	
86	12			94	8	AGWLLSPR	1989	
86	12			94	11	AGWLLSPHGR	1990	
86	12			1858	8	AGVAGVA	1991	
86	12			1858	10	AGVAGVAGA	1992	
86	12	24 0104 40 0089	.	1737	8	ALGLOTA	1993	0.0003
86	12			689	8	ALSTGLIH	1994	
86	12			689	10	ALSTGLIHLH	1995	
79	11			1896	9	ALVVGWCA	1996	
79	11			1896	10	ALVVGWVCAA	1997	
79	11			1793	8	ASLMAFTA	1998	
79	11			2208	10	ASQLSAPSLK	1999	
79	11			2208	11	ASQLSAPSLKA	2000	
86	12			1928	11	ASRCNHSPTH	2001	
100	14			2204	10	ASSASQLSA	2002	
93	13	1090 23	.	165	10	ATGNLPGCSF	2003	0.0260
100	14			1265	8	ATLFGAY	2004	
86	12			1265	11	ATLGAGYMSK	2005	
79	11			48	8	ATHKTSE	2006	
79	11			1596	9	ATVCARAOA	2007	
79	11			1188	8	AVCTRGVA	2008	
79	11			1188	9	AVCTRGVAK	2009	
79	11			1188	10	AVCTRGVAKA	2010	
100	14			1917	10	AVQVMNRLIA	2011	
100	14			1917	11	AVQVMNRLIAF	2012	
93	13			1903	8	CAAILRRH	2013	

Consistency	Freq	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
79	11			1530	9	CAWVELTPA	2014	
93	13			128	9	CGFADLMGY	2015	
79	11			2742	8	CGNTLTCY	2016	
79	11			1130	11	CGSSDLYLVR	2017	
100	14			2727	8	CGYRRCRA	2018	
86	12			2941	11	CLPKLVPPPLR	2019	
100	14			172	9	CSFSIFLA	2020	
100	14			2819	8	CSSNVSA	2021	
86	12			2819	9	CSSNVSAH	2022	0.0001
79	11	1069.62		1128	9	CLGSSULY	2023	
79	11			1190	8	CIRGVAKA	2024	
79	11			1190	11	CIEGVAKAVDF	2025	
79	11			555	9	CTWMNSTGF	2026	
79	11	3.0438		555	11	CTWMNSTGFTK	2027	0.7600
79	11	1.0961		2599	9	CVDFEKGR	2028	0.0008
79	11	1.0501		2599	10	CVDFEKGRK	2029	0.0011
86	12			1462	8	CVTQVDF	2030	
100	14	24.0076		1574	9	DAIFLSQTK	2031	0.0003
79	11			2771	10	DELWICESA	2032	
100	14			1468	8	DFSLDPTF	2033	
79	11			1307	8	DGGGSGGA	2034	
79	11			1307	9	DGKSSGGAY	2035	
86	12			1316	9	LIHICDECH	2036	
86	12			1855	8	DILAGYGA	2037	
79	11			1855	11	DILAGYGAGA	2038	
93	13	1.0144		2617	9	DIGRVCEK	2039	0.0003
93	13			2617	11	DLGVRVCEKMA	2040	
79	11			132	11	DLMGYPLVGA	2041	
79	11			1883	8	DLVNLPA	2042	
79	11			2772	9	DLWICESA	2043	
86	12			1134	8	CLYLVRH	2044	
86	12	24.0074		1134	9	DLYLVRHA	2045	0.0003
79	11			124	8	DLTCGFA	2046	
79	11			1143	8	DVPVRRR	2047	
100	14			2794	8	EAMTRYSA	2048	
79	11			1524	8	E_YUAGJA	2049	
79	11			1524	10	ECYDAGCAWY	2050	
79	11			1882	9	EDLVNLLPA	2051	0.0004
100	14	24.0077		1915	9	EGAVQWMINR	2052	
93	13			1377	8	EIPFYGA	2053	
86	12			2245	8	EMGNITR	2054	
86	12			1342	11	ETAGARLVLA	2055	
86	12			1207	9	ETIMRSPVF	2056	
86	12	1090.24		2596	9	EVFQVDEK	2057	0.0008
79	11			2598	10	FCVDFEKGR	2058	

Accession	Length	Exons	Intron	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
79	11			2598	11	FCVCFSGGJHK	2059	
86	12			1269	8	FGAYNSKA	2060	
86	12			1269	9	FGAYNSKAH	2061	
79	11			553	11	FGCTWNNSTGF	2062	
86	12	1 0.060		2554	9	FGTGAKDVR	2063	0.0008
100	14	40.0082		1773	9	FISGQYLA	2064	
79	11			1304	11	FLVYYSSTGA	2065	
100	14			728	8	FLLADAR	2066	
79	11			2670	8	FSYDTRCF	2067	
100	14			2792	8	FTEAMTRY	2068	
100	14			2792	10	FTEAMTRYSA	2069	
93	13			1567	9	FTGLTHIDA	2070	
93	13			1567	10	FTGLTHIDAH	2071	
93	13			1567	11	FTGLTHIDAHF	2072	
79	11			146	8	GAARALAH	2073	
79	11			146	11	GAARALAHGVR	2074	
86	12			1861	10	GAGVAGALVA	2075	
86	12			1861	11	GAGVAGALVAF	2076	
86	12			350	8	GAHWGVLA	2077	
79	11			1895	10	GALVVGWCA	2078	
79	11			1895	11	GALVVGWCAA	2079	
86	12			1345	8	GARLVLA	2080	
79	11			1345	10	GARLVVLATA	2081	
100	14			1916	8	GAVQWNNR	2082	
100	14			1916	11	GAVQWNNRLIA	2083	
86	12			1270	8	GAYMSKAH	2084	
79	11			1529	10	GCAWYELTPA	2085	
100	14			171	10	GCFSIFLLA	2086	
79	11			554	10	GCTWNNSTGF	2087	
79	11			2770	11	GDLVVICESA	2088	
86	12			278	8	GDLCGSVF	2089	
93	13			129	8	GFADLMGY	2090	
86	12			1268	8	GFGAYMSK	2091	
86	12			1268	9	GFGAYMSKAH	2092	
86	12			1268	10	GFGAYMSKAH	2093	
79	11			2645	9	GFGNSPGR	2094	
79	11			2663	9	GFSYDTRCF	2095	
79	11			145	8	GGAARALA	2096	
79	11			145	9	GGAARALAH	2097	
79	11			1308	8	GGSUGAY	2098	
100	14			26	10	GGGGNGGVY	2099	
79	11			935	8	GGHVVGMA	2100	
100	14			27	9	GGVVGGVY	2101	
100	14	24.0078		1392	9	GGRHUFCH	2102	0.0003
100	14			1392	11	GGRHUFCHSK	2103	

Conservation	Freq	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
79	11			2695	11	GGRPAAIVF	2104	
86	12			1669	8	GGVLAAL A	2105	
86	12			1669	9	GGVLAAL AA	2106	
86	12			1669	10	GGVLAAL AAY	2107	
93	13			32	8	GGVLLPR	2108	
93	13	24-0380		32	9	GGVLLPRR	2109	0.0003
86	12			1818	9	GGWAAOLA	2110	
100	14			1333	9	GIGVLDOA	2111	
79	11			3037	8	GIVLLPNR	2112	
93	13			1552	8	GLPVCOQH	2113	
86	12			1552	11	GLPVCOQHLEF	2114	
79	11			1004	8	GLPVSARR	2115	
79	11			968	8	GLRDILVA	2116	
79	11			2921	8	GLSAFSLH	2117	
79	11			2921	10	GLSAFSLHSY	2118	
100	14	1073-03		1782	10	GLSTLPGNPA	2119	0.0100
93	13			1569	8	GLTHIDAH	2120	
93	13			1569	9	GLTHIDAHF	2121	
86	12			1238	10	GSGKSTKVP A	2122	
86	12			1238	11	GSGKSTKVPAA	2123	
86	12			1131	10	GSSDLYLVTR	2124	
86	12			1131	11	GSSDLYLVTRH	2125	
79	11			2641	8	GSSYGFY	2126	
79	11			2063	8	GTFPINAY	2127	
100	14			1335	10	GTVLDQAE A	2128	
86	12			1863	8	GVAGALVA	2129	
86	12			1863	9	GVAGALVAF	2130	
79	11	1073-10		1863	10	GVAGALVAFK	2131	0.3900
79	11			1193	8	GVAKAVDF	2132	
79	11			1081	8	GVGWTVYH	2133	
79	11			1081	10	GVGWTVYHGA	2134	
79	11	1090-25		3035	10	GVGYLLPNR	2135	0.0014
86	12			1670	8	GVLAALAA	2136	
86	12			1670	9	GVLAALAA Y	2137	0.0046
79	11			45	11	GVRAIRKTSER	2138	
100	14			2619	9	GVRCERMA	2139	
100	14			2619	11	GVRCERMA Y	2140	
86	12			154	11	GVRLDG VNY	2141	
79	11			1900	9	GVVCAAILR	2142	
79	11			1900	10	GVVCAAILRR	2143	
79	11			1900	11	GVVCAAILRRH	2144	
93	13			33	8	GVYLLPRR	2145	
93	13			33	11	GVYLLPRRGR	2146	
79	11			1141	8	HADVIPVR	2147	
79	11			1141	9	HADVIPVR R	2148	



Conservancy	Freq	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
79	11			1141	10	HADVIPRRR	2149	
100	14			1234	8	HAPTGSQK	2150	
93	13			1234	11	HAPTGSQKSTK	2151	
79	11			2920	9	HGLSAFSLH	2152	
79	11			2920	11	HGLSAFSLHSY	2153	
79	11			1624	8	HGPTPLLY	2154	
79	11			1624	9	HGPTPLLYR	2155	
100	14			1572	11	HIDAFLSQTK	2156	
86	12	107316	.	1232	10	HLHW1GSKK	2157	0.5900
79	11			696	11	HLHONVDVOY	2158	
100	14			1395	8	HLIFCHSK	2159	
100	14		.	1395	9	HLIFCHSKA	2160	0.0250
100	14	109026	.	1395	10	HLFLHSKKK	2161	0.0260
93	13	107312		1769	11	HMWN1SGIUY	2162	
100	14			1400	10	HSKKK1DELA	2163	
100	14			1400	11	HSKKK1DELA	2164	
79	11			2928	10	HSYSGEINR	2165	
79	11	11061		222	10	HIPGCVPCVR	2166	0.0004
79	11			1910	8	HVPGEGA	2167	
100	14			1925	9	IAFASRGNIH	2168	
100	14	240074		1573	10	IDAFHLSQTK	2169	
86	12			123	8	IDTLTQGF	2170	
86	12			123	9	IDTLTQFA	2171	
100	14			1397	8	IFCHSKK	2172	
100	14			1334	8	IGTVLDQA	2173	
100	14			1334	11	IGTVLDQAETA	2174	
86	12			1317	8	IICDECH	2175	
79	11	400140		1856	10	ILAGYGAGVA	2176	
86	12			1816	8	ILGGWVA	2177	
86	12			1816	11	ILGGWVAQA	2178	
86	12			1331	11	ILGIGTVLDQA	2179	
86	12			2591	8	IMAKNEVF	2180	
100	14			1774	8	ISGIOYLA	2181	0.0150
86	12	10137	.	2250	9	ITRVESEK	2182	
100	14			2816	11	ITSCSSNVSA	2183	
86	12			989	8	ITWGADTA	2184	
86	12			989	9	ITWGADTAA	2185	
86	12			1296	8	ITYSTYGK	2186	
86	12			1296	9	ITYSTYGK	2187	
79	11			1296	11	ITYSTYGKLA	2188	
86	12			701	8	IVDVLY	2189	
86	12			2613	9	IVFDLQVR	2190	0.0036
79	11	10962		30	10	IVGGVLLPR	2191	0.0008
93	13	11060		30	11	IVGGVLLPRR	2192	
86	12			1736	9	KALGLGTA	2193	

Concurrence	Freq	Peptide	Filled	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
86	12			1404	8	KCEIAAK	2194	
86	12			2553	10	KFGYGAKDVR	2196	
79	11			1391	8	KGGRIHF	2196	
79	11			1391	10	KGGRIHFCH	2197	
79	11			2604	8	KGGKPAR	2198	
86	12			2944	8	KLGVPPIR	2199	
86	12			1241	8	KSTKVPAA	2200	
86	12	13 0016		1241	9	KSTKVPAA*	2201	0 0009
86	12			1241	10	KSTKVPAA*	2202	
79	11			1241	11	KSTKVPAA*	2203	
86	12			10	8	KTKRNTNR	2204	
86	12			10	9	KTKRNTNR	2205	0 0110
93	13	24 0085		51	9	KISERSQPR	2206	0 1600
86	12	1 0952		51	11	KISEHSJHGR	2207	
86	12			121	10	KVIUTLTGFA	2208	
86	12			121	11	KVIUTLTGFA	2209	
100	14			1255	10	KVLVLNPSVA	2210	
100	14			1255	11	KVLVLNPSVA	2211	
79	11			1305	8	KVPAAYAA	2212	
79	11			1305	10	KVPAAYAA	2213	
79	11			1305	11	LADGASGGA	2214	
86	12			1729	8	LAEQFPK	2215	
86	12			1729	9	LAEQFKA	2216	
79	11			1857	9	LAEQFKA	2217	
79	11			1857	11	LAEQFKA	2218	
79	11			1522	10	LAEQFKA	2219	
86	12			1338	9	LDOAETAG	2220	
86	12			1338	10	LDOAETAG	2221	
100	14			727	8	LFIILLADA	2222	
100	14			727	9	LFIILLADA	2223	
86	12			1813	10	LFNLLGWVA	2224	
86	12			1813	11	LFNLLGWVA	2225	
79	11	24 0086		290	8	LFTESPRR	2226	0 0810
86	12			1267	9	LGFAYMSK	2227	
86	12			1267	10	LGFAYMSK	2228	
86	12			1267	11	LGFAYMSK	2229	
79	11			144	9	LGAHAHALA	2230	
79	11			144	10	LGAHAHALA	2231	
86	12			1817	10	LGGWVAAGLA	2232	
93	13			1332	10	LGGTVDGA	2233	
86	12			44	8	LGVRAIRK	2234	
100	14			2618	8	LGVRAIRK	2235	
100	14			2618	10	LGVRAIRK	2236	
100	14			1924	10	LAFASRGNI	2237	
86	12	1 0959		2235	9	LEANLWR	2238	0 0008

Consistency	Freq	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0.001
100	14			1396	8	LIFCHSKK	2239	
100	14	1 0123	.	1396	9	LIFCHSKK	2240	0.5400
79	11			414	9	LNITNGSWH	2241	
79	11	1 1066		2612	10	LIVFDLGWR	2242	0.0003
100	14			1030	8	LLAPITAY	2243	
100	14	24 0071	.	726	9	LLFTLLADA	2244	0.0016
100	14	1090 28	.	726	10	LLFTLLADAR	2245	
86	12			1812	11	LLFNILGWA	2246	
93	13	24 0102		1887	10	LLPAILSPGA	2247	0.0003
93	13			36	8	LLPRRGPR	2248	
86	12			97	8	LLSPRGSR	2249	
79	11			133	10	LMGYIPLVGA	2250	
79	11	13 0019	.	2922	9	LSAFLHSY	2251	0.0002
79	11			2211	8	LSAPSLKA	2252	
86	12			2479	8	LSFSLRH	2253	
86	12	24 0087		2479	9	LSFSLRH#1	2254	0.0003
86	12			690	9	LSTGLHLH	2255	
100	14			1783	9	LSTLFGNFA	2256	
86	12			126	11	LTCGFACLMGY	2257	
100	14			2180	9	LTDPSSHITA	2258	
93	13			1570	8	LTHDAHF	2259	
93	13			2176	10	LTSMLTDFSH	2260	
86	12	40 0133		1591	10	LVAYGATVCA	2261	
79	11			1591	11	LVAYQATVCAR	2262	
79	11			1853	8	LVDILAGY	2263	
79	11	40 0139		1853	10	LVDILAGYGA	2264	
86	12			1667	8	LVGGVLAA	2265	
86	12			1667	10	LVGGVLAALA	2266	
86	12			1667	11	LVGGVLAALAA	2267	
100	14			1257	8	LVINFSVA	2268	
100	14			1257	9	LVLNFSVAA	2269	
79	11			1897	8	LVGWCA	2270	
79	11			1897	9	LVGWVCAA	2271	
79	11			2773	8	LWICESA	2272	
79	11			2668	8	MGFSYDTR	2273	
79	11			2668	10	MGFSYLTHIF	2274	
79	11			2640	9	MGFSYUFOY	2275	
79	11			134	9	MGYPLVGA	2276	
86	12			2876	8	MILMTHFF	2277	
100	14			2179	10	MLTDFSHITA	2278	
79	11	1		1	9	MSTNPKQR	2279	
73	11	1		1	10	MSTNPKPQHP	2280	
79	11	2726		2726	8	NCGYRRCR	2281	
79	11	2726		2726	9	NCGYRRCRA	2282	
79	11	305		305	8	NCSYPGH	2283	

Consistency	Freq	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0303
100	14			1772	8	NFISGIQY	2284	
100	14			1772	10	NFISGIQYLA	2285	
79	11			1080	8	NGVCWTVY	2286	
79	11			1080	9	NGVCWTVYH	2287	
79	11			1080	11	NGVCWTVYHGA	2288	
86	12			1815	8	NILGGWA	2289	
86	12			1815	9	NILGGWAA	2290	
86	12	1 0438		2249	10	NITRVESEHK	2291	0 0010
86	12	1073 01		700	9	NIVDQYLY	2292	0 0005
93	13			1886	11	NLLPAILSPGA	2293	
93	13			168	10	NILPGCSFIF	2294	
86	12			1460	10	NITCVTQTVDK	2295	
79	11			14	10	NINRRPDVK	2296	
79	11	2 0168		14	11	NINRRPDVKF	2297	0 0010
93	13			1549	11	NITPGLFVCDH	2298	
93	13			1889	8	PAILSPGA	2299	
86	12			688	9	PALSTGLIH	2300	
86	12			688	11	PALSTGLIHLH	2301	
79	11			1976	8	PCSGSWLR	2302	
79	11			1127	10	PCITGSSQLY	2303	
93	13			2616	10	PDLGVVCEK	2304	
79	11			1894	11	PGALVGVVCA	2305	
100	14			170	8	PGCSFIF	2306	
100	14			170	11	PGCSFIFLLA	2307	
86	12			224	8	PGCVPLVR	2308	
93	13			1913	11	PGEGAVQMMNR	2309	
79	11			2932	8	PGELNRVA	2310	
86	12			1509	9	PGERPSGMF	2311	
100	14			25	11	PGGGWGGVY	2312	
93	13			1551	9	PGLPVGGJH	2313	
100	14			79	8	PGYWPPLY	2314	
79	11			1295	9	PIITYSTYK	2315	
79	11			1295	10	PIITYSTYKF	2316	
79	11			143	8	PLGGAARA	2317	
79	11			143	10	PLGGAARALA	2318	
79	11			143	11	PLGGAARALAH	2319	
93	13			1628	8	PLLYRLGA	2320	
79	11			2667	9	PMGFSDYIR	2321	
79	11			2667	11	PMKJ SYIHCF	2322	
93	13			514	11	PSPVVVGITDR	2323	
100	14			1261	9	PSVAATLGF	2324	
100	14			1261	11	PSVAATLGFGA	2325	
79	11			1607	8	PSWDMWK	2326	
93	13			587	8	PIDCFRKH	2327	
86	12	1 0954		109	9	PIDFRRSR	2328	0 0008

Compound no.	Length	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
93	13	1 0121		1236	9	PTSGSKSLK	2329	0.0002
86	12			1936	10	PTHVPESDA	2330	
86	12			1936	11	PTHVPESDA	2331	
79	11			1621	11	PTLHGPTPLY	2332	
93	13			1626	10	PTLLYRLGA	2333	
86	12			1554	9	PVQDHLF	2334	
93	13	1 0956		516	9	PVWGIIDR	2335	0.0008
86	12			1340	8	QAEIAGAR	2336	
93	13			1595	8	QATVGARA	2337	
79	11			1595	10	QATVCAHAQA	2338	
93	13			29	11	QINGGVLLPR	2339	
86	12			289	8	QLTFSPR	2340	
79	11	1 0955		289	9	QLTFSPRR	2341	0.7500
86	12			336	8	QLLRIPQA	2342	
79	11			2219	8	QLSAPSLK	2343	
79	11			2210	9	QLSAPSLKA	2344	
86	12			1465	11	QVDFSLDPTF	2345	
79	11			1186	10	RAAVCTRGVA	2346	
79	11			1186	11	RAAVCTRGVAK	2347	
100	14			149	8	RALAHGVR	2348	
79	11			47	9	RATKTSEK	2349	
86	12	24 0088		1930	9	RGNHNSPTH	2350	0.0003
86	12	24 0105		1930	10	RGNHNSPTHY	2351	0.0003
93	13			40	8	RGPRLGVR	2352	
93	13			40	9	RGPRLGVRA	2353	
79	11			40	11	RGPRLGVRATR	2354	
93	13	24 6081		59	9	RGRHJPIK	2355	0.0120
86	12			1154	8	RGLLSPR	2356	
79	11			1192	9	RGVAKVDF	2357	
79	11			43	8	RLGVRATR	2358	
79	11	1073 11		43	9	RLGVRATRK	2359	0.9400
86	12			2918	8	RLHGLSAF	2360	
79	11			2918	11	RLHGLSAFLH	2361	
100	14			1923	8	RLIAFASR	2362	
100	14			1923	11	RLIAFASRGNH	2363	
79	11			2611	11	RLVFPDLGVR	2364	
86	12			1029	8	RLAPITA	2365	
86	12	1174 18		1029	9	RLAPITAY	2366	2.7000
86	12			1347	8	RLVVIATA	2367	
86	12			2875	8	RLMLTHF	2368	
86	12			2875	9	RLMLTHFF	2369	
100	14			635	9	RMVVGVEH	2370	
100	14	1073 13		635	10	RMVVGVEHR	2371	0.7200
93	13			55	8	RSQPRGR	2372	
100	14	1174 21		2621	9	RYCEKNALY	2373	0.1800

Conservancy	Freq	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0.30.1
86	12	1174.17	.	156	9	RVEDGVNR	2374	0.0120
86	12			156	10	RVEDGVNFA	2375	
79	11			2923	8	SAFSLHSY	2376	
79	11			2207	11	SASQLSAPSLK	2377	
100	14			2818	9	SCSSNVSA	2378	
86	12			2818	10	SCSSNVSAH	2379	
86	12			1133	8	SDLYLVTR	2380	
86	12			1133	9	SDLYLVTRH	2381	
86	12			1133	10	SDLYLVTRHA	2382	
100	14			173	8	SFSFLA	2383	
86	12			1239	9	SGKSTKVPFA	2384	
86	12			1239	10	SGKSTKVPAA	2385	
86	12			1239	11	SGKSTKVPAAV	2386	
100	14			2178	8	SMLTDPSTH	2387	
100	14			2178	11	SMLTDPSTHA	2388	
100	14			2206	8	SSASQLSA	2389	
86	12	24.0089		1132	9	SSDLYLVTR	2390	0.0003
86	12	24.0106		1132	10	SSDLYLVTRH	2391	0.0003
86	12			1132	11	SSDLYLVTRHA	2392	
86	12			2820	8	SSNVSAH	2393	
100	14			2205	9	SSASQLSA	2394	
86	12			691	8	STGLJLH	2395	
86	12			1242	8	STKVFAAAT	2396	
86	12			1242	9	STKVFAAATA	2397	
79	11			1242	10	STKVPAATAA	2398	
100	14			1784	8	STLPGNPA	2399	
79	11			2	8	STNPKFOR	2400	
79	11			2	9	STNPKFOR	2401	
79	11			2	11	STNPKFOR	2402	
86	12			1663	11	STNPKFOR	2403	
86	12			1299	8	STNPKFOR	2404	
100	14			1262	8	STNPKFOR	2405	
100	14			1262	10	STNPKFOR	2406	
100	14			1262	11	STNPKFOR	2407	
86	12			1343	10	STNPKFOR	2408	
93	13			127	10	STNPKFOR	2409	
79	11			1129	8	STNPKFOR	2410	
86	12			1461	9	STNPKFOR	2411	
86	12			110	8	STNPKFOR	2412	
100	14			2181	8	STNPKFOR	2413	
79	11			1375	9	STNPKFOR	2414	
79	11			1375	10	STNPKFOR	2415	
93	13			1568	8	STNPKFOR	2416	
93	13	24.0082		1568	9	STNPKFOR	2417	0.0003
93	13			1568	10	STNPKFOR	2418	

Consistency	Eq	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
93	13			166	9	TGNLPGCSF	2419	
93	13			1237	8	TGNAKSLK	2420	
86	12			1237	11	TGSGKSTKPA	2421	
79	11			2590	9	TIMAKNEVF	2422	
86	12	1073 14	.	1266	10	TLGF GATMSK	2423	0 0810
86	12			1266	11	TLGF GATMSKA	2424	
79	11	1073 04	.	1622	10	TLHGPTLLY	2425	0 0890
79	11			1622	11	TLHGPTLLYR	2426	
79	11			686	11	TLPALSTGLIH	2427	
79	11			2871	11	TLWARMILMTH	2428	
100	14			2817	10	TSCSSNVSA	2429	
86	12			2817	11	TSCSSNVSAH	2430	
93	13			52	8	TSESRQR	2431	
86	12	24 0107		52	10	TSESRQRGR	2432	0 0003
86	12			52	11	TSESRQRGR	2433	
86	12			1050	8	TSLTGHOK	2434	
93	13	24 0083		2177	9	TSMITDPSH	2435	0 0003
79	11			2589	10	TTIMAKNEVF	2436	
86	12			1208	8	TTMRSPVF	2437	
79	11			1597	8	TVCARQA	2438	
86	12			1466	10	TVDFSLDPTF	2439	
100	14			1336	9	TVLDOAETA	2440	
86	12			1336	11	TVLDOAETAGA	2441	
100	14			1263	9	VAATLGFGA	2442	
100	14			1263	10	VAATLGFGAY	2443	
86	12			1864	8	VAGALVAF	2444	
86	12	24 0090	.	1864	9	VAGALVAF K	2445	0 2400
86	12	40 0071		1592	9	VAYOATVCA	2446	
79	11	1 1064	.	1592	10	VAYOATVCAR	2447	0 0005
79	11			1592	11	VAYOATVCARA	2448	
79	11			1902	8	VCAAILRR	2449	
79	11			1902	9	VCAAILRRH	2450	
100	14			2622	8	VCEKMALY	2451	
93	13			505	8	VCGPVYCF	2452	
86	12			1555	8	VCOXHEF	2453	
79	11			1189	8	VCTRGVAK	2454	
79	11			1189	8	VCTRGVAKA	2455	
79	11			1082	9	VCVTVYHGA	2456	
100	14			1467	9	VDFSLDPTF	2457	
79	11			1854	9	VDILAGTGA	2458	
93	13			614	9	VDYPRLWH	2459	
93	13			614	10	VDYPRLWHY	2460	
86	12			2597	8	VFCVPEK	2461	
79	11			2597	11	VFCVPEKGR	2462	
79	11			2614	8	VFPDLGVR	2463	

Consistency	Freq	Peptide	Filed	Position	No. of Amino Acids	Sequence	SeqID Num	A*0.30.1
93	13			1566	10	VFTGLTHIDA	2464	
93	13			1566	11	VFTGLTHIDAH	2465	
86	12			277	9	VGDLGGSVF	2466	
86	12			1668	9	VGGVLAALA	2467	
86	12			1668	10	VGGVLAALAA	2468	
86	12			1668	11	VGGVLAALAA	2469	
93	13	24.0084		31	9	VGGVLLPR	2470	0.0003
93	13			31	10	VGGVLLPRR	2471	
79	11			3036	9	VGVLLPNR	2472	0.0007
79	11	1.104.01		1899	10	VGVCAAILR	2473	
79	11			1899	11	VGVCAAILRR	2474	
86	12			122	9	VDTLTGFA	2475	
86	12			122	10	VDTLTGFA	2476	
86	12			1671	8	VLAALAA	2477	
93	13			1521	8	VLCGYDA	2478	
79	11			1521	11	VLCGYDA	2479	
100	14			1337	8	VLDQAEIA	2480	
86	12			1337	10	VLDQAEIAGA	2481	
86	12			1337	11	VLDQAEIAGAR	2482	
86	12			157	8	VLEDGVNY	2483	
86	12			157	9	VLEDGVNYA	2484	
100	14			1258	8	VLNPSVAA	2485	
93	13			2175	11	VLTSMLTDP SH	2486	
79	11			1852	9	VLVDILAGY	2487	
79	11			1852	11	VLVDILAGYGA	2488	
86	12			1666	8	VLGGVLA	2489	
86	12	24.0075		1666	9	VLGGVLA	2490	0.0003
86	12			1666	11	VLGGVLAALA	2491	
100	14	24.0072		1256	9	VLVLNPSVA	2492	0.0003
79	11			1256	10	VLVLNPSVAA	2493	
79	11			2639	8	VMGSSYGF	2494	
79	11			2639	10	VMGSSYGF	2495	
79	11			1138	11	VTRHADIPVR	2496	
79	11			1901	8	VVCAAILR	2497	
79	11			1901	9	VVCAAILRR	2498	
79	11			1901	10	VVCAAILRRH	2499	
79	11			1898	8	VGVVCA	2500	
79	11			1898	11	VGVVCAAILR	2501	
93	13			517	8	VWGTIDR	2502	
86	12			93	9	WAGWLLSFR	2503	
86	12			1766	8	WAKHWNF	2504	
86	12			76	11	WAGPGYWFLY	2505	
86	12			2873	9	WARMILMTH	2506	
86	12			2873	10	WARMILMTHF	2507	
86	12			2873	11	WARMILMTHFF	2508	



Conservative	From	Peptide	File-1	Position	No. of Amino Acids	Sequence	SeqID Num	A*0301
86	12			107	8	WGPTDPRR	2509	
86	12			107	9	WGPTDPRRR	2510	
86	12			107	11	WGPTDPRRRSR	2511	
86	12	1 0953		96	9	WLLSPRGR	2512	0 0008
100	14			1920	8	WMNRLIAF	2513	
100	14	24 0073	.	1920	9	WMNRLIAFA	2514	0 0003
100	14			1920	11	WMNRLIAFSR	2515	
79	11	1174 16	.	557	9	WMNSTGFTK	2516	0 0530
86	12	40 0075		1665	9	WLVGGVLA	2517	
86	12	40 0135		1665	10	WLVGGVLA	2518	
86	12			164	11	YATGNLPGLSF	2519	
79	11			1526	8	YDAGCAWY	2520	
86	12			1315	10	YDIICDECH	2521	
86	12			1860	8	YGAGVAGA	2522	
86	12			1860	11	YGAGVAGALVA	2523	
79	11			2644	10	YGFQYSPGQR	2524	
93	13	1 0951		35	9	YLLPRRGPR	2525	0 0054
86	12			1590	11	YLVAYQATVCA	2526	
79	11			2930	8	YSPGEINR	2527	
79	11			2930	10	YSPGEINRVA	2528	
79	11			2648	9	YSPGQRIFF	2529	
86	12			1298	9	YSTYGKFLA	2530	
86	12			276	10	WGDLCGSVF	2531	
100	14			637	8	YVGVEHR	2532	
86	12			1939	8	YVPESDAA	2533	
86	12			1939	9	YVPESDAAA	2534	
86	12	1 1065		1939	10	YVPESDAAAR	2535	0 0003

Table XVII

HCV All Motif with Binding Information

Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101
AACNWRGER	2536	647	24 0103	10	12	86	0 0140
AARAI AHGVR	2537	147		10	11	79	
AATLGFAY	2538	1264		9	14	100	
AAVLTREYAK	2539	1187		10	11	79	
ACNWRGER	2540	648		9	12	86	
AKKFSQAY	2541	1306		10	11	79	
ALVIVRR	2542	1142		8	12	86	
ALVIVRRR	2543	1142		9	11	79	
ALASRNIH	2544	1926		8	14	100	
AGALVAFK	2545	1865		8	12	86	
AGVAAALVAIK	2546	1862		11	12	86	
AGWLTSPH	2547	94		8	12	86	
AGWLTSPKSR	2548	94		11	12	86	
ALITGLIH	2549	689	24 0104	8	12	86	0 0027
ALSTLPHH	2550	689		10	12	86	
ASQISAPSLK	2551	2208		10	11	79	
ASRGPRVSPH	2552	1928		11	12	86	
ATLGRGAY	2553	1265		8	14	100	
ATLGRGAYMSK	2554	1265		11	12	86	
ATHKTSR	2555	48		8	11	79	
AVLTREYAK	2556	1188	1090 23	9	11	79	0 0250
CAAEIRRH	2557	1903		8	13	93	
CGFALIMGY	2558	128		9	13	93	
CLNLTGLY	2559	2742		8	11	79	
CGSSRLVLR	2560	1130		11	11	79	
CLRKGVPLR	2561	2041		11	12	86	
CNLSIPGH	2562	304		9	11	79	
CAWTHGER	2563	649		8	12	86	
CSSNVVAH	2564	2819		9	12	86	
CICGSSLY	2565	1128	1069 62	9	11	79	0 0063
CLWNNSLGRK	2566	555	3 0438	11	11	79	0 7500
CVAFKGRK	2567	2599	1 0961	9	11	79	0 0005
CVAFKGRK	2568	2599	1 0501	10	11	79	0 0008
DAFLSQTK	2569	1574	24 0076	9	14	100	0 0005
DCKFSQAY	2570	1307		9	11	79	
DIHIDECH	2571	1316		9	12	86	0 0002
DGVNCEK	2572	2617	1 0144	9	13	93	
DIYLVRH	2573	1134		8	12	86	
DVIVRRR	2574	1143		8	11	79	
EGTAAICAWY	2575	1524		10	11	79	
EGAVQMMNR	2576	1915	24 0077	9	14	100	0 0014
EMGNITR	2577	2145		8	12	86	
EVFVCEK	2578	2596	1090 24	9	12	86	0 0270
FLVAFKGRK	2579	2598		10	11	79	
FOVFERGRK	2580	2598		11	11	79	

Sequence	Length (nm)	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101
FGAYMSKAH	2581	1269		9	12	86	
FGYCAKQVR	2582	2554	1 0960	9	12	86	0 0005
FLILADAR	2583	728		8	14	100	
FLFAMTFY	2584	2792		8	14	100	
FLGTHQAH	2585	1567		10	13	93	
GAARALAH	2586	146		8	11	79	
GAARALAHGVR	2587	146		11	11	79	
GAVCWMPR	2588	1916		8	14	100	
GAVMKAH	2589	1270		8	12	86	
GAALMAY	2590	129		8	13	93	
GFAYMSK	2591	1268		8	12	86	
GFAYMSKAH	2592	1268		10	12	86	
GFVYKQAR	2593	2645		9	11	79	
GGARALAH	2594	145		9	11	79	
GGSSGAY	2595	1308		8	11	79	
GGKAGVY	2596	26		10	14	100	
GGKAGVY	2597	27		9	14	100	
GGRIIFCI	2598	1392		9	14	100	0 0001
GGRIIFCSK	2599	1392	24 0078	11	14	100	
GGVLAALAY	2600	1669		10	12	86	
GGVILPR	2601	32		8	13	93	
GGVILPRR	2602	32	24 0080	9	13	93	0 0010
GVIIPNR	2603	3037		8	11	79	
GLPVXXH	2604	1552		8	13	93	
GLPVSAAR	2605	1004		8	11	79	
GLSAFLH	2606	2921		8	11	79	
GLSAFLHSY	2607	2921	1073 03	10	11	79	0 0005
GLTHDAH	2608	1569		8	13	93	
GNHVSPT	2609	1931		8	12	86	
GNVSPHY	2610	1931		9	12	86	
GNTRVEFNK	2611	2248		11	12	86	
GSSDYLVTIR	2612	1131		10	12	86	
GSSDYLVTIRH	2613	1131		11	12	86	
GSSGFGY	2614	2641		8	11	79	
GTFPINAY	2615	2063		8	11	79	
GVAGAVAK	2616	1863	1073 10	10	12	86	1 4000
GVCMVYH	2617	1081		8	11	79	
GVGVILPVR	2618	3035	1090 25	10	11	79	0 0140
GVLAALAY	2619	1670	1174 19	9	12	86	0 0110
GVRAIRKISR	2620	45		11	11	79	
GVRCFKALY	2621	2619		11	14	100	
GVRLDGNY	2622	154		11	12	86	
GVVCAILIR	2623	1900		9	11	79	
GVVCAILIRH	2624	1900		10	11	79	
GVVCAILIRH	2625	1900		11	11	79	

Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101
GWYLLPRR	2626	33		8	13	93	
GWYLLPRGPR	2627	33		11	13	93	
HADVIVRR	2628	1141		8	11	79	
HADVIVRR	2629	1141		9	11	79	
HADVIVRRH	2630	1141		10	11	79	
HAPTGSCK	2631	1234		8	14	100	
HAPTGSCKSTK	2632	1234		11	13	93	
HCLSAFSLH	2633	2920		9	11	79	
HCLSAFSLHSY	2634	2920		11	11	79	
HCPTEPLY	2635	1624		8	11	79	
HCPTEPLYR	2636	1624		9	11	79	
HIDAHLSQTK	2637	1572		11	14	100	
HIHAPTGSCK	2638	1232	1073 16	10	12	86	0 0024
HIHONIVQY	2639	696		11	11	79	
HIHGHCK	2640	1395		8	14	100	
HIHGHSPK	2641	1305	1090 26	9	14	100	0 0006
HIHGHSPK*	2642	1395	1073 12	10	14	100	0 0002
HMWNFSGQY	2643	1769		11	13	93	
HSYSPGENR	2644	2928		10	11	79	
HIHGVQVQVR	2645	222	1 1061	10	11	79	0 0012
IAFASRGNI	2646	1925	24 0079	9	14	100	0 0003
IDAHLSQTK	2647	1573		10	14	100	
IFGHKKK	2648	1397		8	14	100	
IICDELCH	2649	1317		8	12	86	
ININGSWH	2650	415		8	11	79	
ITRVESENK	2651	2250	1 0137	9	12	86	0 0079
IT*STGK	2652	1296		8	12	86	
IVDGYLY	2653	701		8	12	86	
IVPDGVH	2654	2613		9	11	79	
IVGGVYLLPR	2655	30	1 0962	10	13	93	0 0044
IVGGVYLLPHR	2656	30	1 1060	11	13	93	0 0056
KCELAALK	2657	1404		8	12	86	
KFAGAKDVH	2658	2553		10	12	86	
KGGHHLFCH	2659	1391		10	11	79	
KGLHKKPAH	2660	2604		8	11	79	
KLGVPPLH	2661	2944		8	12	86	
KHEVGVJFEK	2662	2594		11	11	79	
KSTKVPAAV	2663	1241	13 0016	9	12	86	0 0001
KTKRNTIR	2664	10		8	12	86	
KTKRNTIRH	2665	19	24 0085	9	12	86	0 0100
KLSRQJPR	2666	51	1 0952	9	13	93	0 0640
KTSRSQPRGR	2667	51		11	12	86	
LADYFSSJAY	2668	1305		11	11	79	
LAQFQK	2669	1729		8	12	86	
LDOAETAGAR	2670	1338		10	12	86	

Sequence	SeqID Num	Position	Peptide No	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*11101
LELLADAR	2671	727		9	12	100	
LEHSHRH	2672	290		8	11	79	
LEFGVMSK	2673	1267	24 0086	9	12	86	0.2900
LEFGVMSKAH	2674			11	12	86	
LEGAARALAH	2675	144		10	11	79	
LEGRATRK	2676	44		8	12	86	
LEMGCEK	2677	2618		8	12	100	
LEMAAGGNH	2678	1924		10	14	100	
LEMLLWR	2679	2235	1 0959	9	12	86	0.0005
LEFGSKK	2680	1396		8	14	100	
LECEKKEK	2681	1396	1 0123	9	14	100	0.1900
LEINFGSWH	2682	414		9	11	79	
LEMPFGVR	2683	2612	1 1066	10	11	79	0.0001
LEAPLAY	2684	1030		8	14	100	
LELLADAR	2685	726	1090 28	10	14	100	
LEFRGGR	2686	36		8	13	93	
LESFGSH	2687	97		8	12	86	
LESAFSLHSY	2688	2922		9	11	79	0.0002
LESRLRH	2689	2479	13 0019	8	12	86	
LESGLRRH	2690	2479	24 0087	9	12	86	0.0001
LEGLRH	2691	690		9	12	86	
LEGFALMGY	2692	126		11	12	86	
LEMLTDPFH	2693	2176		10	13	93	
LEVAGATVCAR	2694	1591		11	11	79	
LEVILAGY	2695	1853		8	11	79	
MEFSYDTR	2696	2668		8	11	79	
MESSGFQI	2697	2640		9	11	79	
MNRLAFASR	2698	1921		10	14	100	
MNLTGFK	2699	558		8	11	79	
MSINFKPOR	2700	1		9	11	79	
MSINFKFQK	2701	1		10	11	79	
NGGFRGR	2702	2726		8	11	79	
NCSTFGH	2703	305		8	11	79	
NFISGIGY	2704	1772		8	14	100	
NGVQWTVY	2705	1080		8	11	79	
NGVQWTVYH	2706	1080		9	11	79	
NHVESENK	2707	2249	1 0498	10	12	86	0.0062
NVLVQHLT	2708	709	1073 01	9	12	86	0.0140
NHRRKQDVK	2709	14	2 0168	10	11	79	0.0007
NHFGPVQDDH	2710	1549		11	13	93	
PALSTGLH	2711	688		9	12	86	
PALSTGLHH	2712	688		11	12	86	
PCGCSMLR	2713	1976		8	11	79	
PCGCSQLY	2714	1127		10	11	79	
PDGVRVCEK	2715	2616		10	13	93	

Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*11101
PLGVPCVR	2716	224		8	12	86	
PLGVAVWMK	2717	1913		11	13	93	
PLGVAVKGV	2718	25		11	14	100	
PLGVVQKH	2719	1551		9	13	93	
PLGVWFLY	2720	79		8	14	100	
PLVSLYVK	2721	1295		9	11	79	
PLGVAAALAH	2722	143		11	11	79	
PLVPSYDTR	2723	2667		9	11	79	
PLVILGVR	2724	1281		8	13	93	
PLVPSYDTR	2725	514		11	13	93	
PLVPSYDTR	2726	1607		8	11	79	
PLVPSYDTR	2727	587		8	13	93	
PLVPSYDTR	2728	109	1 0954	9	12	86	0 0005
PLVPSYDTR	2729	1236	1 0121	9	13	93	0 0001
PLVPSYDTR	2730	1621		11	11	79	
PLVPSYDTR	2731	516	1 0956	9	13	93	0 0005
PLVPSYDTR	2732	1340		8	12	86	
PLVPSYDTR	2733	29		11	13	93	
PLVPSYDTR	2734	289		8	12	86	
PLVPSYDTR	2735	289	1 0955	9	11	79	0 0330
PLVPSYDTR	2736	2210		8	11	79	
PLVPSYDTR	2737	699		8	11	79	
PLVPSYDTR	2738	699		10	11	79	
PLVPSYDTR	2739	1186		11	11	79	
PLVPSYDTR	2740	149		8	14	100	
PLVPSYDTR	2741	47		9	11	79	
PLVPSYDTR	2742	1930	24 0088	9	12	86	0 0001
PLVPSYDTR	2743	1930	24 0105	10	12	86	0 0001
PLVPSYDTR	2744	40		8	13	93	
PLVPSYDTR	2745	40		11	11	79	
PLVPSYDTR	2746	59	24 0081	9	13	93	0 0017
PLVPSYDTR	2747	1154		8	12	86	
PLVPSYDTR	2748	43	1073 11	8	11	79	0 0290
PLVPSYDTR	2749	43		9	11	79	
PLVPSYDTR	2750	2918		11	11	79	
PLVPSYDTR	2751	1923		8	14	100	
PLVPSYDTR	2752	1923		11	12	100	
PLVPSYDTR	2753	2611	1174 18	11	11	79	0 0270
PLVPSYDTR	2754	1029		9	12	86	
PLVPSYDTR	2755	635	1073 13	9	14	100	0 0200
PLVPSYDTR	2756	635		10	14	100	
PLVPSYDTR	2757	13		11	11	79	
PLVPSYDTR	2758	55		8	13	93	
PLVPSYDTR	2759	2621	1174 21	9	14	100	0 5000
PLVPSYDTR	2760	156	1174 17	9	12	86	0 0068

Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101
SAPGLPSY	2761	2923		8	11	79	
SAPGLSAPSEK	2762	2707		11	11	79	
SLSNVSAH	2763	2818		10	12	86	
SLQYIVTR	2764	1133		8	12	86	
SLRYIVTRH	2765	1133		9	12	86	
SLKSLKVPAAV	2766	1239		11	12	86	
SMILTPSA	2767	2178		8	14	100	
SNRLTHH	2768	2480		8	12	86	
SNRYIVTR	2769	1132	24 0089	9	12	86	0 0044
SNRLYIVTRH	2770	1132	24 0106	10	12	86	0 0013
SNVSAH	2771	2820		8	12	86	
SLGLHH	2772	691		8	12	86	
SLKFAAY	2773	1242		8	12	86	
SLNPKPQR	2774	?		8	11	79	
SLNPKYQRK	2775	?		9	11	79	
SLNPKFJRKTK	2776	?		11	11	79	
SVAAILGFAY	2777	1262		11	14	100	
TLGLALHMG	2778	127		10	13	93	
TLGLSSDLY	2779	1129		8	11	79	
TLPTFRSR	2780	110		8	12	86	
TLGPFYK	2781	1375		9	11	79	
TLGLTHDAH	2782	1568	24 0082	9	13	93	0 0001
TLGSGKSTK	2783	1237		8	13	93	
TLGLAYMSK	2784	1266	1073 14	10	12	86	0 0610
TLGLFIPLLY	2785	1622	1073 04	10	11	79	0 0007
TLHGKPTLYR	2786	1622		11	11	79	
TLPALSTGLH	2787	686		11	11	79	
TLWARMILMTH	2788	2871		11	11	79	
INPKPQRK	2789	3		8	11	79	
INPKPQRTPK	2790	3		10	11	79	
INPKFGRTPR	2791	3		11	11	79	
INRFQGVK	2792	15		9	11	79	
ISLSNVSAH	2793	2817		11	12	86	
ISLRSPQR	2794	52		8	13	93	
ISLRSPQRGR	2795	52	24 0107	10	12	86	0 0001
ISLRSPQRGRH	2796	52		11	12	86	
ISLIGRDK	2797	1050		8	12	86	
ISMLTPSAH	2798	2177	24 0083	9	13	93	0 0001
VAAILGFAY	2799	1263		10	14	100	
VAGALVAFK	2800	1864	24 0090	9	12	86	0 8930
VATVALVCAH	2801	1592	1 1064	10	11	79	0 0038
VCAAILRR	2802	1902		8	11	79	
VLAAILHHH	2803	1902		9	11	79	
VCEKALALY	2804	2622		8	14	100	
VQTRVAK	2805	1189		8	11	79	

Sequence	SeqID Num	Position	Peptide No	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101
VDPYRWH	2806	614		9	13	93	
VDPYRWHY	2807	614		10	13	93	
VICVETK	2808	2597		8	12	86	
VICVETKGR	2809	2597		11	11	79	
VIFVGR	2810	2614		8	11	79	
VIGLIDDAH	2811	1566		11	13	93	
VIGVLAALAAV	2812	1668		11	12	86	
VIGVYLER	2813	31	24 0084	9	13	93	0 0019
VIGVYLFRR	2814	31		10	13	93	
VIGVYLFRR	2815	3036	F104 01	9	11	79	0 0100
VIGVYLFRR	2816	1899		10	11	79	
VIGVYLAALRR	2817	1899		11	11	79	
VLAALAAV	2818	1671		8	12	86	
VLDQAE TAGAR	2819	1337		11	12	86	
VLEXVNY	2820	157		8	12	86	
VLSMLTDPSSH	2821	2175		11	13	93	
VLDLAGY	2822	1852		9	11	79	
VMLSSYGFQY	2823	2639		10	10	79	
VIRHADVIVR	2824	1138		11	11	79	
VVCAALR	2825	1901		8	11	79	
VVCAALRR	2826	1901		9	11	79	
VVCAALRRH	2827	1901		10	11	79	
VVGVCAALR	2828	1898		11	11	79	
VVGTIDR	2829	517		8	13	93	
WAGWLLSPR	2830	93		9	12	86	
WAGFGTPWPI	2831	76		11	12	86	
WARMILMH	2832	2873		9	12	86	
WGPTDPRR	2833	107		8	12	86	
WGPTDPRR	2834	107		9	12	86	
WGPTDPRRSR	2835	107		11	12	86	
WLSPRCSR	2836	96	1 0953	9	12	86	0 0005
WMNRILAFSR	2837	1920		11	14	100	
WMNSTGFIR	2838	557	1174 16	9	11	79	0 0810
WNFISGIY	2839	1771		9	14	100	
YDAGCAWY	2840	1526		8	11	79	
YLAIDECH	2841	1315		10	12	86	
YGFQSPQAR	2842	2644		10	11	79	
YLPFRGFR	2843	35	1 0951	9	13	93	0 0005
YSPGFRR	2844	2930		8	11	79	
YVAVRR	2845	637		8	14	100	
YVFESDAAR	2846	1939	1 1065	10	12	86	0 0001



Table XVIII

HCV A24 Motif with Binding InformationTable XVIII HCV A24 Motif With Binding Information

Frequency	Peptide	Isolated	Position	Sequence	SeqID Num	A*2401	Motif
86			319	AWDMMNW	2847		A241
79	13 0132		1248	AYAAQYKVL	2848	0 0609	A241
100			1421	AYRGLDVSI	2849		A241
79			1525	CYDAGCAW	2850		A241
79			1525	CYDAGCAWYEL	2851		A241
100			1468	DFSLOPIF	2852		A241
14			1468	DFSLOPFTI	2853		A241
86	24 0092	1996	1765	FWAKHWNJF	2854	6 9000	A241
86			1765	FWAKHWNJF	2855		A241
93			129	GFADLMGYI	2856		A241
79			129	GFADLMGYPL	2857		A241
79			2669	GFSDYTRCF	2858		A241
79			1027	GWRLAPI	2859		A241
86	13 0133		1859	GYGAGVAGAL	2860	0 0003	A241
79	13 0131		135	GYPLVAGAPL	2861	0 0057	A241
86			2728	GYRRCRASJVL	2862		A241
93	1174 08	1996	1769	HMMNFISGI	2863		A241
86			176	IFLLALLSCL	2864		A241
86			2591	IMAKNEVF	2865		A241
93			23	KPGGGGI	2866		A241
86			1813	LTHLGW	2867		A241
86			2872	LWARMILMTHF	2868		A241
86			2241	LWRJEMGGJH	2869		A241
79			1135	LYLVTRHADVI	2870		A241
100			1770	MWNFISGI	2871		A241
14			1770	MWNFISGIQYL	2872		A241
93	1073 18	1993	636	MYVGGVEHRL	2873	0 0270	A241
100	24 0091	1996	1772	NFISGIQYL	2874	0 0170	A241
79			2667	PMGFSYDTRCF	2875		A241
86			1732	QFKQKALGL	2876		A241
86			1732	QFKQKALGLL	2877		A241
14			1919	QWNNRLIAF	2878		A241
100	13 0075	1995	1778	QYLAGLSTL	2879	0 0480	A241
79	13 0134	1995	2647	QYSPGQVFF	2880	0 0180	A241
79			2647	QYSPGQVFFL	2881		A241
86			317	RMWDMMNW	2882		A241
12			2875	RMILMTHF	2883		A241
86			2875	RMILMTHFF	2884		A241
93			635	RMVVGVEHLL	2885		A241
14			173	SFSIFLLAL	2886		A241
100	24 0108		173	SFSIFLLAL	2887	0 0041	A241
14	1174 10		2178	SMLTDPShi	2888		A241
100			1608	SWDMMKCL	2889		A241
79			1164	SYLKGSSGGPL	2890		A241
86			556	TWNINSTGF	2891		A241
79							A241

Conservation	Freq	Peptide	Filed	Position	Sequence	SeqID Num	A*2401	Motif
86	12			1664	TWLVGGVL	2892		A241
93	13			1297	LYSTGGKF	2893		A241
86	12		1995	1297	LYSTGGKEL	2894	0.0230	A241
93	13	13.0074		1566	VETGLHI	2895		A241
79	11			2639	VMSSGAF	2896		A241
93	13	1073.19	1993	34	VYLLFRGGPRL	2897	0.0016	A241
100	14			1920	WMRLIAF	2898		A241
100	14			1422	YYRGLDVSIV	2899		A241

Table XIXa HCV DR-Super Motif Binding Data Not Included

Core Sequence	Core SeqID Num	Core Freq.	Core Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position in Poly-protein	Peptide No.	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
FGAYMSKAI	3052	12	86	TLGFGAYMSKAIIGVD	2900	1266		5	36
FGCTWMSST	3053	12	86	GNWFGCTWMSSTGFT	2901	550	1283.13	11	79
FKQKALGLL	3054	12	86	AEQFKQKALGLLQTA	2902	1730	1283.35	12	86
FTLALLSCL	3055	12	86	FSIELLALLSCLTVP	2903	174		6	43
FPIDIGRVVC	3056	11	79	LIVFPDILGVRVCFKM	2904	2612		11	79
FQVAHLHAP	3057	12	86	PQTFQVAHLHAPTGS	2905	1225	1283.19	6	43
FRAAYCTRG	3058	12	86	VGFRAAYCTRGVAK	2906	1182		7	50
FSILLALL	3059	14	100	GCFSFSIFLALLSCL	2907	171	1283.09	12	86
FSIDPFIET	3060	14	100	IVDFSLDPFIETIT	2908	1466	1283.28	11	79
FTEAMIRYS	3061	14	100	LRVFTEAMIRYSAPP	2909	2789		7	50
FIPSPVAVG	3062	13	93	VYCFIPSPVAVGTTD	2910	509	1283.12	13	93
FUTIPALST	3063	11	79	PCSFUTIPALSTGLJ	2911	681		9	64
FWAKHMAWNE	3064	12	86	LEVFWAKHMAWNEISG	2912	1762		3	21
HDALHLSQT	3065	14	100	LTHIDALHLSQTKQA	2913	1570		7	50
HDNCTCTQ	3066	12	86	DSVIDNCTCTQTVD	2914	1454	1283.27	12	86
HDLLFCGEA	3067	12	86	GKVIDLLFCGEADLM	2915	120		12	86
HEANLLWRQ	3068	12	86	ADLHEANLLWRQEMG	2916	2233		7	50
HLIALLSC	3069	14	100	SFSIELLALLSCLTV	2917	173		6	43
HLGGWVAAQ	3070	12	86	LENILGGWVAAQLAP	2918	1813		8	57
HLGIGVLD	3071	12	86	STILGIGVLDQAE	2919	1328		8	57
HLRPHVGP	3072	11	79	CAAHHLRPHVGPGEA	2920	1903	1283.42	11	79
HLSPGALVV	3073	13	93	LPAILSPGALVVGAV	2921	1888		11	79
INAYTTGPC	3074	12	86	TFPINAYTTGPCIPS	2922	2064		8	57
IPLVGAPLG	3075	11	79	MGYIPLVGAPLGGAA	2923	134		10	71
IRVSENRK	3076	12	86	GGNIRVSENRKVVI	2924	2247		10	71
ITSCSSNVS	3077	14	100	LELITSCSSNVSAIH	2925	2813	1283.57	11	79
IVFPDIGVR	3078	11	79	ARTIVFPDIGVRVCF	2926	2610	1283.52	11	79
LAALAAAYCL	3079	12	86	GGVLAALAAAYCLTTG	2927	1669		8	57
LADGGCSGG	3080	11	79	GKFLADGGCSGGAYD	2928	1302		10	71
LAGLSLTPG	3081	14	100	IQYLAGLSLTPGNPA	2929	1777	1283.37	14	100
LAGYGAGVA	3082	11	79	VDILAGYGAGVAGAL	2930	1854		10	71
LATAIPPGS	3083	12	86	LVVLATATIPPGSVTV	2931	1348		9	64
LDPFTFIEF	3084	12	86	DFSLDPTFIEFTTV	2932	1468		5	36
LDQAEIACA	3085	12	86	GTVLDQAEIAGARLV	2933	1335	1283.23	12	86

Table XIXa HCV DR-Super Motif Binding Data Not Included

Core Sequence	Core SeqID Num	Core Freq.	Core Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position In HCV Poly-protein	Peptide No.	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
LEHISCSS	3086	13	93	EYDELEITSCSSNV	2934	2810		13	93
LEVVLSTWV	3087	12	86	SADLEVVTSTWVLVG	2935	1655		11	79
LEFLADAR	3088	14	100	VVLLFLLADARVCS	2936	724	1283.15	4	29
LGGWVAAQL	3089	12	86	FNILGGWVAAQLAPP	2937	1814		8	57
LGIGTVLDQ	3090	13	93	TTILGIGTVLDQAET	2938	1329		9	64
LGVRATRKI	3091	12	86	GPRLGVRATRKTSER	2939	41		10	71
LGVRVCEKM	3092	14	100	FPDLGVRVCEKMALY	2940	2615	1283.53	11	79
LHGLSAFSL	3093	11	79	IERLHGLSAFSLHSY	2941	2916		6	43
LHGPTPLY	3094	11	79	KPTLHGPTPLYRLG	2942	1620	1283.32	11	79
LHQNIQDVQ	3095	12	86	LIHLHQNIQDVQYLY	2943	694		10	71
LHYSPPGEL	3096	11	79	AFSLHYSPPGENRV	2944	2924	1283.60	11	79
LIAFASRGN	3097	14	100	MNRLLIAFASRGNHVS	2945	1921	1283.44	12	86
LILANLWR	3098	12	86	DADLIEANLWRQFM	2946	2232	1283.47	7	50
LHCHSKKK	3099	14	100	GRHLIFCHSKKKCDE	2947	1393	1283.25	14	100
LIISCSSNV	3100	14	100	DLELITSCSSNVSA	2948	2812		13	93
LLALLSCLT	3101	12	86	SIFLLALLSCLTTPA	2949	175		5	36
LEFLFLADA	3102	14	100	YVVLLEFLFLADARVC	2950	723		5	36
LEFNILGGW	3103	12	86	QNTTLEFNILGGWVAA	2951	1809		4	29
LLADARVC	3104	13	93	LLFLLADARVCACL	2952	726		9	64
LEPAILSPG	3105	13	93	LVNLLPAILSPGALV	2953	1884		10	71
LEMGYPLVAG	3106	11	79	FADLMGYPLVAGAPL	2954	130		11	79
LEPSVAATL	3107	14	100	VLVLNPSVAATLGFG	2955	1256	1283.22	14	100
EPAILSPGA	3108	13	93	VNLLPAILSPGALVV	2956	885		11	79
EPALSTGLI	3109	12	86	FTTLPALSTGLIHJH	2957	684	1283.14	11	79
LEPRGPRI G	3110	13	93	VYLLPRGPRI GLVRA	2958	34	1283.02	13	93
LRDI AVAVE	3111	11	79	HNGLRDLAVAVEPVV	2959	966		4	29
LPKTCVPII	3112	12	86	ASCLRKLGVPPPLRVW	2960	2939	1283.61	7	50
LSAFSLHSY	3113	11	79	LHGLSAFSLHSYSPG	2961	2919	1283.59	11	79
LSAPSLKAI	3114	11	79	ASQLSAPSLKATCTT	2962	2208	1283.46	7	50
LSNSLIRIH	3115	12	86	INALSNSLIRIHNMV	2963	2476		4	29
LEPGALVVG	3116	13	93	PAILSPGALVVGVC	2964	1889		11	79
LSPIILSTI	3117	11	79	RSFISPIILSTTEWQ	2965	664		7	50
LEPRGSRPS	3118	11	79	GWLLSPRGSRPSWGP	2966	95		11	79
LESLGLIHJH	3119	12	86	LPALSTGLIHJHJNI	2967	687		10	71

Table XIXa IICV DR-Super Motif Binding Data Not Included

Core Sequence	Core SeqID Num	Core Freq.	Core Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position In IICV Poly-protein	Peptide No.	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
LTCGEADLM	3120	12	86	IDTLTCGEADLMGYI	2968	123	1283.05	12	86
LTHDAHFL	3121	13	93	FTGLTHDAHFLSQI	2969	1567	1283.30	13	93
LTSMLTDPHS	3122	13	93	VAVLTSMLTDPHSHT	2970	2173		9	64
LVAAYQATVC	3123	12	86	FPYLVAYQATVCARA	2971	1588		9	64
LVDILAGYGG	3124	11	79	GKVLVDILAGYGGAV	2972	1850		9	64
LXGGVLAAL	3125	12	86	TWVLXGGVLAALAAAY	2973	1664	1283.34	12	86
LVLNPSVAA	3126	14	100	YKVLVLNPSVAATLG	2974	1254		14	100
LVLNLPAIL	3127	11	79	TEDVLNLPAILSPG	2975	1881		10	71
LVTIRHADVI	3128	11	79	DLVLVTIRHADVIPVR	2976	1134	1283.17	11	79
LVGGVVCAA	3129	11	79	PGALVVGGVVCAAILR	2977	1894		11	79
LVLATATIP	3130	12	86	GARLVVLATATIPPGS	2978	1345	1283.24	11	79
LWARMILMT	3131	12	86	APTLWARMILMTTHFF	2979	2869		11	79
LWQJENGGN	3132	12	86	ANLLWQJENGGNITR	2980	2238	1283.48	12	86
LYRIGAVQN	3133	11	79	TPLLYRIGAVQNEVT	2981	1627		9	64
MAENEVECV	3134	12	86	THMAKNEVECVQPE	2982	2389	1283.51	9	64
MAWDMMINW	3135	12	86	GHRMAWDMMINWSPT	2983	315	1283.10	12	86
MGGNTRVF	3136	12	86	RQEMGGNTRVESEN	2984	2243	1283.49	12	86
MGYIPLVGA	3137	11	79	ADLMGYIPLVGAPLG	2985	131	1283.06	11	79
MLTDPSHIT	3138	14	100	LTSMLTDPSHITAET	2986	2176	1283.45	8	57
MNRIIAFAS	3139	14	100	VQWMNRIIAFASRGN	2987	1918		14	100
MTRYSAAPG	3140	14	100	TEAMTRYSAAPGDPP	2988	2793		10	71
MWNFISGIG	3141	14	100	AKHMWNFISGHQYLA	2989	1767	1283.36	12	86
MYVGGVPHR	3142	14	100	KVRMYVGGVPHRLNA	2990	633		5	36
VAGALVAFK	3143	12	86	GAGVAGALVAFKVMIS	2991	1861		7	50
VAHLIAPITG	3144	12	86	TFQVAHLIAPITGSGK	2992	1227		6	43
VATDALMTG	3145	12	86	VVVVATDALMTGYTG	2993	1437	35.0106	6	43
VAYQATVCA	3146	12	86	PYLVAYQATVCAARAQ	2994	1589		11	79
VCAALIRRH	3147	11	79	VGVVCAALIRRHIVGP	2995	1899		10	71
VCEKMAIYD	3148	14	100	GVRVCEKMAIYDVVS	2996	2619	1283.54	11	79
VCCDHLEFW	3149	12	86	GLPYCCDHLEFWESV	2997	1552	35.0109	6	43
VCTRGVAKA	3150	11	79	RAAVCTRGVAKAVDF	2998	1186	1283.18	11	79
VFCVQPEKG	3151	12	86	KNEVFCVQPEKGGRE	2999	2594		10	71
VFTDNSSPP	3152	11	79	RSPVFTDNSSPPAVP	3000	1211		10	71
VFTGLTHID	3153	13	93	WESVFTGLTHIDAHIF	3001	1563	1283.29	6	43

Table XIXa HCV DR-Super Motif Binding Data Not Included

Core Sequence	Core SeqID Num	Core Freq.	Core Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position In HCV Poly-protein	Peptide No.	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
VGGVLAALA	3154	12	86	WVLVGGVLAALAAYC	3002	1665		12	86
VGGVYLLPR	3155	13	93	GQIVGGVYLLPRRGP	3003	28		13	93
VGSQLPCEP	3156	12	86	QYLVSQLPCEPEPD	3004	2158		6	43
VGVVCAAIL	3157	11	79	ALVGVVCAAILRRH	3005	1896		11	79
VIDCNTCVT	3158	12	86	FDSVIDCNTCVTQIV	3006	1453		12	86
VIDLTCGF	3159	12	86	LKGVIDTLTCGFADL	3007	119	1283.04	11	79
VLAALAAYC	3160	12	86	VGGVLAALAAYCLTT	3008	1668		8	57
VLATAIPPG	3161	13	93	RLVLATAIPPGSVT	3009	1347		9	64
VLEDGVNYA	3162	12	86	GVRVLEDGVNYATGN	3010	154	1283.07	12	86
VLNPSVAAT	3163	14	100	KVLVLNPSVAATLGF	3011	1255		14	100
VLTSMHTDP	3164	13	93	DVAVLTSMHTDPSHH	3012	2172		9	64
VLTSCGNT	3165	11	79	ASGVLTTSCGNTLTC	3013	2734		10	71
VLYDILAGY	3166	11	79	LKGVLVDILAGYGAG	3014	1849		10	71
VLYGGVLA	3167	12	86	STWVLVGGVLAALAA	3015	1663		12	86
VLYNPSVA	3168	14	100	GYKVLVLYNPSVAATL	3016	1253	1283.21	14	100
VNLIPAILS	3169	12	86	EDLVNLIIPAILSPGA	3017	1882	1283.39	11	79
VPESDAAAR	3170	12	86	THYVPESDAAARVTQ	3018	1937		7	50
VTESTAWVVG	3171	12	86	LEVVTSTWVLVGGVL	3019	1658	1283.33	12	86
VVAIDALMT	3172	11	79	DVVVVATDALMTGYT	3020	1436	1283.26	6	43
VVC AAILRR	3173	11	79	VVGVC AAILRRHVIG	3021	1898		10	71
VGVVVC AAI	3174	11	79	GALVVGVVVC AAILRR	3022	1895	1283.41	11	79
VVIATAIPP	3175	12	86	ARLVVLTATAPPGSV	3023	1346		9	64
VYGFIPSPV	3176	13	93	CGPVYGFIPSPVVVG	3024	506	1283.11	13	93
WAGWTLSPR	3177	12	86	GCGWAGWLLSPRGR	3025	90		5	36
WARMHMTTH	3178	12	86	PTLWARMHMTTHFFS	3026	2870	1283.58	11	79
WGADTAACG	3179	12	86	IITWGADTAACGDII	3027	988		6	43
WGTPDPRRR	3180	12	86	RPSWGPDPRRRSRN	3028	104		10	71
WMNRLIAFA	3181	14	100	AVQWMNRLIAFASRG	3029	1917	1283.43	14	100
WRLLAPITA	3182	11	79	SKGWRLIAPITAYAQ	3030	1025	1283.16	4	29
WIGALLTFC	3183	11	79	SYTWTGALLTFCAAE	3031	2456	1283.50	9	64
WYELIPAFI	3184	12	86	GCAWYELTPAETTVR	3032	1529		5	36
YATGNLPGC	3185	12	86	GVNYATGNLPGCSFS	3033	161	1283.08	11	79
YCFIPSPVV	3186	13	93	GPVYCFIPSPVVVGT	3034	507		13	93
YDAGCAWYEL	3187	11	79	CECYDAGCAWYELTP	3035	1523		10	71

Table XIXa HCV DR-Super Motif Binding Data Not Included

Core Sequence	Core SeqID Num	Core Freq	Core Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position In HCV Poly-protein	Peptide No.	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
YDIHDFC	3188	12	86	GGAYDIIICDECHST	3036	1312		10	71
YDIETHSC	3189	13	93	QPEYDLELITSSSN	3037	2808	1283.56	11	79
YGAGVAGAL	3190	12	86	LAGYGAGVAGALVAF	3038	1857	1283.38	11	79
YGFQYSPGQ	3191	11	79	GSSYGQYSPGQVE	3039	2641	1283.55	10	71
YGFELADGG	3192	11	79	YSTYGKFLADGGCSG	3040	1298		10	71
YKVLVLNPS	3193	14	100	AQGYKVLVLNPSVAA	3041	1251	1283.20	11	79
YLAGLSLTP	3194	14	100	GIQYLAGLSLTPGNP	3042	1776		14	100
YLGSSGGP	3195	12	86	PVSYLKSSGGPLLC	3043	1162		6	43
YLRDPTTP	3196	11	79	RVYYI TRDPTTP IAR	3044	2833		9	64
YQATVCARA	3197	13	93	LVAYQATVCARAQAP	3045	1591		11	79
YRGLDVSVI	3198	14	100	VAYYRGLDVSVIPTS	3046	1420		7	50
YRLGAVQNE	3199	11	79	PLLYRLGAVQNEVTL	3047	1628		9	64
YRRCRASGV	3200	13	93	NCGYRRCRASGVLT	3048	2726		10	71
YSHEPLDLP	3201	11	79	GACYSHEPLDLPQII	3049	2902		6	43
YSPGFNRV	3202	11	79	LHSYSPGFNRVASC	3050	2927		8	57
YVGDICGSV	3203	12	86	SAMYVGDICGSVFLV	3051	273	35.0103	8	57
VGYTLIPNR	3204	11	79			3036	080.02		





### Table XIX B

[illegible]



Table XXa HCV DR 3A Motif Binding Data Not Included

Core Sequence	Core SeqID Num	Core Freq	Core Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position In Hc V Poly-protein	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
HLADGGSG	3205	11	79	YGKELADGGCGGAY	3224	1301	10	71
ESLDPTFTT	3206	14	100	TVDFSLDPTFTTFT	3225	1466	11	79
LEGEPCDDP	3207	14	100	MPPLGEGPCDDLS	3226	2401	11	79
LPCLPEPDAV	3208	12	86	GSQPCPEPDAVAVL	3227	2162	9	64
MAWDMMMSW	3209	12	86	GHRMAWDMMMSWPT	3228	315	12	86
MLTDSHLL	3210	14	100	LTSMLTDSHLLTFT	3229	2176	8	57
MSADLEAVT	3211	11	79	MACMSADLEAVTSTW	3230	1651	6	43
VADDAIMIG	3212	12	86	VVVVATDALMTGYTG	3231	1437	6	43
VCQDHLFTW	3213	12	86	GLPVCQDHLFEWESV	3232	1552	6	43
VFPHLCARV	3214	11	79	RLVFPDLGVRVCEK	3233	2611	11	79
VFDNSSP	3215	11	79	RSPVFTONSSPAVP	3234	1211	10	71
VFLCYDAG	3216	13	93	DSSVLCFCYDAGCAW	3235	1518	10	71
VLFDAVNYA	3217	12	86	GVRVLEDGVNYATGN	3236	154	12	86
VLADEAGV	3218	11	79	LGRVLDILAGYGAG	3237	1849	10	71
VQPEKGGRK	3219	11	79	VFCVQPEKGGKKPAR	3238	2597	11	79
YDIETTFSC	3220	13	93	QPFYDIETTFSCSSN	3239	2808	11	79
YSHPPLDLP	3221	11	79	GACYSHPPLDLPQII	3240	2902	6	43
YVGDLCGSV	3222	12	86	SAMVVGDLCSVFLV	3241	273	8	57
YVPSIDAAA	3223	12	86	PTHVVPESDAAARVT	3242	1936	12	86



Table XXc HCV 3B Motif

Core Sequence	Core SeqID Num	Core Freq	Core Conservancy (%)	Exemplary Sequence	Exemplary SeqID Num	Position In HCV Poly-protein	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)
ECUSKKCD	3243	14	100	HLIFCHSKKKCDELA	3250	1395	14	100
ESYDTRCED	3244	11	79	PMGFSYDTRCFDSTV	3251	2667	11	79
LAFOIKOKA	3245	12	86	GMQLAEQFKQKALGL	3252	1726	8	57
LKPTLHGPT	3246	11	79	LIRLKPILLHGPTLL	3253	1616	10	71
VRATRKISE	3247	11	79	RLGVRATBKTSFSSQ	3254	43	10	71
YLVTRIADV	3248	12	86	SDLVLVTRIADVIPV	3255	1133	11	79
MSISNKPQR	3249		79			1		

### HCV 3B Motif Binding Data

Table XXd

[illegible]

Table XXII  
HCV Analogs

AA	Sequence	SeqID Num	Fixed Nomen	A1 Motif	A2 Super Motif	A3 Super Motif	A24 Motif	B7 Super Motif	1 Anchor Fixer
9	RVXKMLY	3642		N	N	Y	N	N	No
9	AVXTHGVAK	3643		N	N	Y	N	N	
9	LVXVGPER	3644		N	N	Y	N	N	
9	HLIFVHSPK	3645		N	N	Y	N	N	
9	IPGXSF SIF	3646		N	N	Y	N	Y	
9	LFVHSKKK	3647		N	N	Y	N	N	
10	VLAALAAAYXI	3648		N	Y	N	N	N	No
10	HLIFVHSPKK	3649		N	N	Y	N	N	
10	AAXNWTRGER	3650		N	N	Y	N	N	
10	TLPRRGPRV	3651	12 LV10	N	Y	N	N	N	1
9	IPGXSF SIF	3652		N	N	N	N	Y	
9	IPVCSF SIF	3653		N	N	N	N	Y	
9	IPGXSF SIF	3654		N	N	N	N	Y	
9	IPGXSF SIF	3655		N	N	N	N	Y	
9	IPGXSF SIF	3656		N	N	N	N	Y	
9	IPGXSF SIF	3657		N	N	N	N	Y	
9	IPGXSF SIF	3658		N	N	N	N	Y	
9	IPGXSF SIF	3659		N	N	N	N	Y	
9	PPVWHGCP	3660		N	N	N	N	Y	
10	KP'LEHGP'IT'	3661		N	N	N	N	Y	
10	APTLWARMI	3662		N	N	N	N	Y	
9	SPRGSHF'SI	3663		N	N	N	N	Y	
10	IPRGPRIGI	3664		N	N	N	N	Y	
9	SPGXRVET	3665		N	N	N	N	Y	
9	IPGXSF SIF	3666		N	N	N	N	Y	
9	DPRRSRRI	3667		N	N	N	N	Y	No
10	SPGALWGV	3668		N	N	N	N	Y	No
10	TPLLYRLGAI	3669		N	N	N	N	Y	No
9	ISGVLWGV	3670		N	Y	N	N	N	No
9	SISGVLWGV	3671		N	Y	N	N	N	No
9	SI MAFTASV	3672		N	Y	N	N	N	No
9	GLDGTMLV	3673		N	Y	N	N	N	No
10	KI VALGVNAV	3674		N	Y	N	N	N	No
10	ILP'SRGPKL	3675		N	Y	N	N	N	No
10	KISGLGVNAV	3676		N	Y	N	N	N	No
10	VLPRGPRL	3677	LV2 110	N	Y	N	N	N	Rev
10	VFNILGGW	3678		N	N	N	N	N	No
10	KLVSLGVNAV	3679	12 VA9	N	Y	N	N	N	Rev
9	CINGVWTA	3680	1A2 V9	N	Y	N	N	N	Rev
9	CANFVWTV			N	Y	N	N	N	

HCV ANALOGS

AA	Sequence	SeqID Num	Fixed Nomen	A1 Motif	A2 Super Motif	A3 Super Motif	A24 Motif	B7 Super Motif	1 Anchor Fixer
9	CVNGVCWAV	3681		N	Y	N	N	N	



Supermotif	Peptide	Seq ID	Sequence	Protein	Position	Immunogenicity						
						Barnaba <sup>a</sup>		Human <sup>a</sup>			Transgenic mice <sup>b</sup>	
						patients	contacts	Chisari	Pape	overall	Frequency	Response
A2	1073 05	3256	FLFNILGGWV	NS4	1812	1/6	7/17	2/21	0/6	10/50	6/6	6.4 (1.7)
	1090 18	3257	FLLLADARV	NS1/E2	728	2/6	7/17	1/21	0/6	10/50	5/6	9.5 (3.0)
	1013 02	3258	YLVAAYQATV	NS4	1590	1/6	4/17	1/21	0/6	6/50	5/6	8.5 (3.7)
	1090 22	3259	RLVFPDLGV	NS5	2578	2/6	5/17	0/21	0/6	7/50	0/6	-
	1013 1002	3260	DEMGVPLV	Core	132	2/6	7/17	1/21	1/6	11/50	5/6	8.8 (2.6)
	21 0073	3261	WNNRLIAFA	NS4	1920	1/6	3/17	2/21	1/6	7/50	0/6	-
	21 0075	3262	VLVGGVLA	NS4	1666	1/6	6/17	3/21	1/6	11/50	0/6	-
	1174 08	3263	HNWNFESGI	NS4	1769	3/6	3/17	2/21	0/6	8/50	6/6	6.4 (1.7)
	1073 06	3264	LLAGYGAGV	NS4	1851	2/6	3/17	0/21	0/6	5/50	3/6	54.7 (3.3)
	1073 07	3265	YLI PRRGPR	CORE	35	2/6	5/17	7/21	1/6	17/50	4/6	59.1 (7.2)
	21 0071	3266	LLFLLLADA	NS1/E2	726	2/6	9/17	0/21	0/6	11/50	0/6	-
	1 0119	3267	YLVTRHADV	NS3	1131	6/6	10/17	0/21	1/6	17/50	0/6	-
A3	1 0952	3268	KTSERSQPR	CORE	51	2/16	1/4	3/12	0/6	6/38	3/6	23.4 (1.3)
	1073 11	3269	RLGVRATRK	CORE	43	4/16	1/4	7/12	1/6	13/38	3/6	42.2 (1.2)
	1 0955	3270	QLFTESPR	ENV	290	1/16	0/4	6/12	1/6	8/38		
	1073 13	3271	RMVVGGVTHR	NS1/E2	632	5/16	1/4	4/12	1/6	11/38	2/6	2.8 (1.1)
	1 0123	3272	LHCHSKKK	NS3	1396	6/16	1/4	4/12	2/6	13/38	3/6	4.4 (1.1)
	1073 10	3273	GVAGALVAFK	NS4	1863	3/16	0/4	6/12	2/6	11/38	6/6	56.5 (1.7)
B7	21 0090	3274	VAGALVAFK	NS4	1864	4/16	1/4	6/12	0/4	11/38	1/6	7.1
	21 0086	3275	TLCFGAYMSK	NS3	1262	6/16		2/12	2/5	10/33		
	1145 12	3276	LPGCSFSIF	CORE	169			2	3/10	5		

Table XXIV. Human and murine MHC-peptide binding assays established using purified MHC molecules and gel filtration chromatography

Species		Antigen	Allele	Cell line	Radiolabeled peptide			Notes
					Source	Seq ID	Sequence	
Human	A1	A*0101	Steinlin	Hu J chain 102-110		3277	YTAVVPLVY	no NEN in PI cocktail
	A2	A*0201	JY	HBBc 18-27 F6->Y		3278	FLPSDYFPSV	"
	A2	A*0202	P815 (transfected)	HBBc 18-27 F6->Y		3279	FLPSDYFPSV	"
	A2	A*0203	FUN	HBBc 18-27 F6->Y		3280	FLPSDYFPSV	"
	A2	A*0206	CLA	HBBc 18-27 F6->Y		3281	FLPSDYFPSV	"
	A2	A*0207	721.221 (transfected)	HBBc 18-27 F6->Y		3282	FLPSDYFPSV	"
	A3		GM3107	non-natural (A3CON1)		3283	KVEPYALINK	"
	A11		BVR	non-natural (A3CON1)		3284	KVEPYALINK	"
	A24	A*2402	KAS116	non-natural (A24CON1)		3285	AYIDNYNKF	"
	A31	A*3101	SPACH	non-natural (A3CON1)		3286	KVEPYALINK	"
	A33	A*3301	LWAGS	non-natural (A3CON1)		3287	KVEPYALINK	"
	A28/68	A*6801	C1R	HBBc 141-151 T7->Y		3288	STLPETYVVR	"
	A28/68	A*6802	AMAI	HBB pol 646-654 C4->A		3289	FTQAGYPAL	"
	B7	B*0702	GM3107	A2 sigal seq. 5-13 (L7->Y)		3290	APRTILVYLL	"
	B8	B*0801	Steinlin	HVgp 586-593 Y1->F, Q5->		3291	ELKDYQLL	"
	B27	B*2705	LC2	R 60s		3292	FRYNGILIR	"
	B35	B*3501	C1R, BVR	non-natural (B35CON2)		3293	FPKYAAAF	"
	B35	B*3502	TISI	non-natural (B35CON2)		3294	FPKYAAAF	"
	B35	B*3503	EHM	non-natural (B35CON2)		3295	FPKYAAAF	"
	B44	B*4403	PTOUT	EF-1 G6->Y		3296	AEMGKYSFY	"
	B51		KAS116	non-natural (B35CON2)		3297	FPKYAAAF	"
	B53	B*5301	AMAI	non-natural (B35CON2)		3298	FPKYAAAF	"
	B54	B*5401	KT3	non-natural (B35CON2)		3299	FPKYAAAF	"
	Cw4	Cw*0401	C1R	non-natural (C4CON1)		3300	QYDIDAVYKI	"
	Cw6	Cw*0602	721.221 transfected	non-natural (C6CON1)		3301	YRHDXGNVL	"
	Cw7	Cw*0702	721.221 transfected	non-natural (C6CON1)		3302	YRHDXGNVL	"
Mouse	D <sup>b</sup>		EL4	Adenovirus E1A P7->Y		3303	SGPSNTYPEI	"
	K <sup>b</sup>		EL4	VSV NP 52-59		3304	RGYVFCGL	"
	D <sup>d</sup>		P815	HIV-1HB ENV G4->Y		3305	RCPYRAFVTI	"
	K <sup>d</sup>		P815	non-natural (KdCON1)		3306	KFNPMKLYI	"
	I <sup>d</sup>		P815	HBBs 28-39		3307	IPQSLDSYWTSL	"

Table XXIV. Human and murine MHC-peptide binding assays established using purified MHC molecules and gel filtration chromatography

Species	Antigen	Allele	Cell line	Radiolabeled peptide		Notes
				Source	Sequence	
Human	DR1	DRB1*0101	IC2	HA Y307-319	YPRYVKQNILKLAT	
	DR2	DRB1*1501	I466.1	MBP 88-102Y	VVHFFKNIVTPRTPPY	
	DR2	DRB1*1601	I242.5	non-natural (760.16)	YAAFAAAKTAATAFA	
	DR3	DRB1*0301	MAT	MT 65KD Y3-13	YKTIAFDEEAR	optimal assay pH is 4.5
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	YARFQSQTTLKQKT	
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	YARFQRQTTLKAAA	
	DR4w14	DRB1*0404	BIN 40	non-natural (717.01)	YARFQSQTTLKQKT	
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	YARFQSQTTLKQKT	
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKFFGITE	
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKFFGITE	
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKFFGITE	
	DR9	DRB1*0901	IID	Tet. tox. 830-843	QYIKANSKFFGITE	
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	QYIKANSKFFGITE	
	DR12	DRB1*1201	Herluf	unknown eluted peptide	EALIHQLKINPYVLS	
	DR13	DRB1*1302	I40301	Tet. tox. 830-843 S->A	QYIKANAKFFGITE	
	DR51	DRB5*0101	GM3107 or I416.3	Tet. tox. 830-843	QYIKANAKFFGITE	
	DR51	DRB5*0201	I255.1	HA 307-319	PKYVKQNTLKLAT	
	DR52	DRB3*0101	MAT	Tet. tox. 1272-1284	NGQICNDPNRDIL	
	DR53	DRB4*0101	I257.6	non-natural (717.01)	YARFQSQTTLKQKT	no NEM in PI mix
	DQA1	DQA1*0301/DQB1*0301	PF	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	
Mouse	IA <sup>b</sup>		DR27.4	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	optimal assay pH is 5.5
	IA <sup>d</sup>		A20	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	
	IA <sup>e</sup>		CH-12	HEL 46-61	YNIDGSDYGLQINSR	optimal assay pH is 5.0
	IA <sup>c</sup>		LS102.9	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	
	IA <sup>a</sup>		91.7	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	
	II <sup>d</sup>		A20	Lambda repressor 12-26	YLEDARRKAIYEKKK	optimal assay pH is 5.0
	II <sup>e</sup>		CH-12	Lambda repressor 12-26	YLEDARRKAIYEKKK	optimal assay pH is 5.0

Table XXVI: HCV-derived conserved high algorithm A\*0201-binding peptides

Peptide	Molecule	1st Position	Seq ID	Sequence	Consv.	A2-supertype binding capacity (IC <sub>50</sub> nM)					
						A*0201	A*0202	A*0203	A*0206	A*6802	A2 XRN
1073.05	NS4	1812	3335	LLFNILGGWV	85	4.2	113	3.2	19	33	5
1090.18	NS1/E2	728	3336	FLLLADARV	92	18	90	149	247	111	5
1013.02	NS4	1590	3337	YLVAYQATV	85	20	39	16	82	33	5
1090.22	NS5	2611	3338	RLVFPDLGV	79	56	391	10	370	8000	4
1013.1002	CORE	132	3339	DLMGYPLV	79	80	4778	204	481	12	4
24.0073	NS4	1920	3340	WMNRLLAFA	100	122	130	3.3	1609	400	4
24.0075	NS4	1666	3341	VLVCGVLAA	85	185	331	32	308	3077	4
1174.08	NS4	1769	3342	IMWNTISCI	92	15	10750	77	132	7547	3
1073.06	NS4	1851	3343	ILAGYGAGV	79	116	143	5.0	755	889	3
1073.07	CORE	35	3344	YLLPRRCPR	92	125	6143	455	416	10256	3
24.0071	NS1/E2	726	3345	LLFLLADA	100	217	287	455	3364	3077	3
1.0119	LORE	1131	3346	YLVTRHADV	85	455	2048	3.6	71	3077	3
24.0065	NS4	1891	3347	ILSPGALVV	92	238	10750	27	1028	3077	2
1013.12	NS1/E2	686	3348	ALSTGLIHL	85	313	7167	45	18500	10256	2
939.14	NS1/E2	696	3349	HLHQNIVDV	85	500	3071	19	1370	10811	2
1090.21	NS5	2918	3350	RLHGLSAFSL	79	179	782	625	18500	12500	1

Table XXVII: HCV-derived conserved high algorithm A\*03 and/or A\*11 binding peptides

Peptide	Molecule	1st Position	Seq ID	Sequence	Consv.	A3-supertype binding capacity (IC <sub>50</sub> nM)						
						A*03	A*11	A*3101	A*3301	A*6801	A*3 XRN	
1.0952	CORE	51	3364	KTSESSQPR	92	69	94	67	1813	145	4	
1073.11	CORE	43	3365	RLGVRATRK	79	12	207	429	-	-	3	
1.0955	ENV1	290	3366	QLFTFSPRR	79	15	182	621	3766	3	3	
1073.13	NS1/E2	632	3367	RMVYVGVEHIR	100	15	300	95	9667	1778	3	
1.0123	NS3	1396	3368	HLFCHSKKK	100	20	32	2535	24167	333	3	
1073.10	NS4	1863	3369	GVAGALVAFK	85	28	4	3273	26364	118	3	
24.0090	NS4	1864	3370	VAGALVAFK	85	46	7	3750	11600	258	3	
24.0086	NS3	1262	3371	LGFGAYMSK	85	136	21	2950	22308	222	3	
1174.16	NS1/E2	557	3372	WMNSTGFTK	79	208	74	12857	690	1429	2	
1073.14	NS3	1261	3373	TLGFGAYMSK	85	136	98	-	22308	8889	2	
1090.23	CORE	1183	3374	AVCTRGVAK	79	423	240	16364	-	-	2	
1090.24	NS5	2596	3375	EVFCVQPEK	85	13750	222	-	-	18	2	
24.0103	NS1/E2	647	3376	AACNWTRGER	85	36667	429	400	5273	4444	2	
1073.16	NS3	1232	3377	HLIAPTCSGK	85	19	2500	-	-	2857	1	
1073.12	NS3	1395	3378	HLIFCHSKKK	100	423	-	20000	-	-	1	
1090.26	NS3	1395	3379	HLIFCHSKK	100	440	10000	-	-	8000	1	

\* A dash indicates IC<sub>50</sub>nM >30,000

Table XXVIII: HCV derived conserved B\*0702 binding peptides

## A. High conservancy 9- and 10-mer peptides.

Peptide	Molecule	1st Position	SEQ ID	Sequence	Consv.	B7-supertype binding capacity (IC <sub>50</sub> nM)						
						B*0702	B*3501	B*51	B*5301	B*5401	B7 XRN	
1145.12	Core	169	3380	LPGCSFSIF	92	28	90	100	114	6667	4	
15.0048	E2	681	3381	LPALSTGLI	85	157	-	2.8	1500	20000	2	
15.0234	NS3	1620	3382	KPTLHGPTPL	79	3.9	-	27500	-	-	1	
15.0247	NS5	2835	3383	APTLWARMIL	79	6.3	-	5500	-	-	1	
15.0042	CORE	99	3384	SPRGSRPSW	79	14	-	11000	-	-	1	
15.0039	Core	57	3385	QPRGRRQPI	92	24	-	-	-	-	1	
15.0218	Core	37	3386	LPRRGPRIGV	92	29	-	6111	-	4000	1	
15.0060	NS5	2615	3387	SPGQRVHEL	79	46	-	27500	-	-	1	
15.0043	Core	111	3388	DPRRSRNIL	85	324	-	-	-	-	1	
15.0063	NS5	2835	3389	APTLWARMIL	79	344	-	4583	-	-	1	
1292.17	NS5	2317	3390	PPVVHGCPL	79	393	-	-	-	-	1	
15.0239	NS4	1893	3391	SPGALVVGAV	79	423	-	3438	-	-	1	
15.0235	NS3	1621	3392	TPLLYRIGAV	92	458	-	6875	-	909	1	

Table XXVIII: HCV derived conserved B\*0702 binding peptides

## B. Additional HCV derived B7 supermotif peptides.

Peptide	Molecule	1st Position	SEQ ID	Sequence	Consv.	B7-supertype binding capacity (IC <sub>50</sub> nM)					
						B*0702	B*3501	B*51	B*5301	B*5401	B7 XRN
29.0035	NS3	1378	3393	IPFYGKAI	92	458	-	46	-	50	3
29.0040	Core	37	3394	LPRRGPRIL	92	0.85	-	306	-	5000	2
29.0036	Core	137	3395	IPLVGAPL	79	13	2250	79	-	2857	2
16.0187	NS1/E2	680	3396	LPGSFITLPA	64	423	24000	9167	-	15	2
29.0039	Core	169	3397	LPGCSFSI	92	500	200	932	620	6250	2
15.0219	Core	142	3398	APLGGAAARAL	71	9.5	-	-	-	12500	1
29.0031	NS5	2869	3399	APTLWARM	79	13	-	4583	-	4348	1
15.0231	NS3	1512	3400	RPSGMFDSSV	71	153	-	-	-	-	1
29.0085	NS5	2474	3401	LPINALSNL	57	220	18000	1170	-	11111	1
29.0037	NS5	2608	3402	KPARLIVF	85	367	-	3235	-	16667	1
15.0237	NS4	1789	3403	NPAIASLMAF	71	393	9000	5000	-	-	1
29.0118	NS5	2869	3404	APTLWARMILM	79	423	-	-	-	3030	1
29.0042	NS4	1720	3405	LPYIEQGM	85	423	-	1375	-	7692	1

## C. Engineered analogs of B7 supermotif peptides.

Peptide	Molecule	1st Position	SEQ ID	Sequence	Consv.	B7-supertype binding capacity (IC <sub>50</sub> nM)					
						B*0702	B*3501	B*51	B*5301	B*5401	B7 XRN
1145.12	Core	169	3406	LPGCSFSIF	92	28	90	100	114	6667	4
1292.24	Core	169	3407	LPGCSFSII		37	4364	5.3	262	1056	3
1145.13	Core	169	3408	FPGCSFSIF		19	1.6	132	3.2	6.7	5

\* A dash indicates IC<sub>50</sub> nM >30,000.

**Table XXIX: HCV-derived A1- and A24-motif containing peptides****A. A1-motif peptides**

Peptide	Molecule	Position	Seq ID	Sequence	Conserv.	HLA-A*0101 binding (IC50 nM)
13.0019	NS5	2922	3409	LSAFSLHSY	79	31
1.0509	NS5	2921	3410	GLSAFSLHSY	79	61
1069.62	NS3	1128	3411	CTCGSSDLY	79	68
24.0093	NS5	2129	3412	EVDGVR LHRY	100	167
13.0016	NS3	1241	3413	KSTKVPAAAY	85	1923
1.0125	NS3	1525	3414	CYDAGCAWY	79	4032
24.0008	E1	206	3415	DCSNSSIVY	85	16667
24.0094	NS5	2720	3416	TNSKGQNCGY	100	-
24.0096	NS3	1240	3417	GKSTKVPAAAY	85	-
24.0100	NS3	1292	3418	TGAPITYSTY	85	-
	NS3	1263	3419	VAAITLGFGAY	100	-
	NS5	2639	3420	VMGSSYGFQY	79	-
	NS5	2640	3421	MGSSYGFQY	79	-

A dash indicates IC50 nM &gt;25000

**B. A24 -motif peptides**

Peptide	Molecule	Position	Seq ID	Sequence	Conserv.	HLA-A*2402 binding (IC50 nM)
24.0092	NS4	1765	3422	FWAKHMWNF	85	1.7
13.0075	NS4	1778	3423	QYLAGLSTL	100	250
1073.18	NS1 E2	636	3424	MYVGGVEHRL	92	444
13.0074	NS3	1297	3425	TYSTYGKFL	85	522
13.0134	NS5	2647	3426	QYSPGQRVEF	79	667
24.0091	NS4	1772	3427	NFISGIQYL	100	706
13.0131	Core	135	3428	GYIPLVGAPL	79	2105
24.0108	Core	173	3429	SFSIFLLALL	100	2927
13.0132	NS3	1248	3430	AYAAQGYKVL	79	13333
13.0133	NS4	1859	3431	GYGAGVAGAL	85	-
1174.08	NS4	1769	3432	HMWNFISGI	93	-
	E1	317	3433	RMAWDMMMNW	85	-
	NS1 E2	635	3434	RMVVGVEHRL	93	-
	NS3	1422	3435	YYRGLDVSVI	100	-
	NS3	1468	3436	DFSLDPTFTI	100	-
	NS3	1608	3437	SWDQMWKCL	79	-
	NS3	1664	3438	TWVLVGGVL	85	-
	NS4	1732	3439	QFKQKALGL	85	-
	NS4	1732	3440	QFKQKALGLL	85	-
	NS4	1765	3441	FWAKHMWNFI	85	-
	NS4	1919	3442	QWMNRLIAF	100	-
	NS5	2241	3443	LWRQEMGGNI	85	-
	NS5	2669	3444	GFSYDTRCF	79	-
	NS5	2875	3445	RMILMTHFF	85	-

A dash indicates IC50 nM &gt;25000



Table XXX: Immunogenicity of A2-supertype cross-reactive binders

Immunogenicity												
Human <sup>a</sup> Transgenic mice <sup>b</sup>												
Barnaba; Barnaba;												
Peptide	Seq ID	Sequence	Protein	Position	patients	contacts	Chisari	Pape	overall	Frequency	Response	
1073.05	3446	LLFNILGGWV	NS4	1812	1/6	7/17	2/21	0/6	10/50	6/6	6.4 (1.7)	
1090.18	3447	FLLADARV	NS1/E2	728	2/6	7/17	1/21	0/6	10/50	5/6	9.5 (3.0)	
1013.02	3448	YLVAYQATV	NS4	1590	1/6	4/17	1/21	0/6	6/50	5/6	8.5 (3.7)	
1090.22	3449	RLVFPDGV	NS5	2578	2/6	5/17	0/21	0/6	7/50	0/6	-	
1013.1002	3450	DLMGYIPLV	Core	132	2/6	7/17	1/21	1/6	11/50	5/6	8.8 (2.6)	
24.0073	3451	WMNRLLAF	NS4	1920	1/6	3/17	2/21	1/6	7/50	0/6	-	
24.0075	3452	VLVGGVLA	NS4	1666	1/6	6/17	3/21	1/6	11/50	0/6	-	
1174.08	3453	HIMWNFISGL	NS4	1769	3/6	3/17	2/21	0/6	8/50	6/6	6.4 (1.7)	
1073.06	3454	ILAGYGGAGV	NS4	1851	2/6	3/17	0/21	0/6	5/50	3/6	54.7 (3.3)	
1073.07	3455	YLLPRRGPRLL	CORE	35	2/6	5/17	7/21	1/6	17/50	4/6	59.1 (7.2)	
24.0071	3456	LLFLLADA	NS1/E2	726	2/6	9/17	0/21	0/6	11/50	0/6	-	
10119	3457	YLVTRIADV	NS3	1131	6/6	10/17	0/21	1/6	17/50	0/6	-	

a. Data shown represents the number of positive responses over the total number of patients or contacts examined.

b. Frequency represents the number of positive responses over the total number of mice examined. Response indicates the average magnitude (standard deviation) of the response in positive animals, measured in lytic units.

Table XXXI: Immunogenicity of A3-supertype cross-reactive binders

Peptide	SEQ ID	Sequence	Protein	Position	Immunogenicity				
					Human <sup>a</sup>		Transgenic mice <sup>b</sup>		
					Barnaba patients	Barnaba contacts	Chisari	Pape	overall
1.0952	3458	KTSERSQPR	CORE	51	2/16	1/4	3/12	0/6	6/38
1073.11	3459	RLGVRAIRK	CORE	43	4/16	1/4	7/12	1/6	13/38
1.0955	3460	QLFTFSPRR	ENV	290	1/16	0/4	6/12	1/6	8/38
1073.13	3461	RMYYVGGVTHR	NS142	632	5/16	1/4	4/12	1/6	11/38
1.0123	3462	LHFCIISKKK	NS3	1396	6/16	1/4	4/12	2/6	13/38
1073.10	3463	GVAGALVAFK	NS4	1863	3/16	0/4	6/12	2/6	11/38
24.0090	3464	VAGALVAFK	NS4	1864	4/16	1/4	6/12	0/4	11/38
24.0086	3465	TLGFGAYMSK	NS3	1262	6/16		2/12	2/5	10/33

a. Data shown represents the number of positive responses over the total number of patients or contacts examined.

b. Frequency represents the number of positive responses over the total number of mice examined. Response indicates the average magnitude (standard deviation) of the response in positive animals, measured in lytic units.

Table XXXII. Candidate HCV-derived HTL epitopes

Selection criteria	Peptide	SEQ ID	Sequence	Source	Conservancy	
					Total	Core
A DR-supermotif conserved 15mers	1283.01	3641	GQIVGGVYLLPRRGPR	HCV Core 28	93	93
	1283.02	3466	VYLLPRRGPRILGVRA	HCV Core 34	93	93
	1283.03	3467	GWLLSPRGSRPSWGPT	HCV Core 95	79	79
	1283.04	3468	LGKVIDTLTCGFADL	HCV Core 119	79	86
	1283.05	3469	IDTLTCGFADLMGYI	HCV Core 123	86	86
	1283.06	3470	ADLMGYIPLVGAPLG	HCV Core 131	79	79
	1283.07	3471	GVRVIEDGVNYATGN	HCV Core 154	86	86
	1283.08	3472	GVNYATGNLPGCSFS	HCV Core 161	79	86
	1283.09	3473	GCSFSIFLLALLSCL	HCV Core 171	86	100
	1283.10	3474	GHRMAWDMMMNWSPT	HCV E1 315	86	86
	1283.11	3475	CGPVYCFPSPVVVG	HCV NS1 E2 506	93	93
	1283.12	3476	VYCFPSPVVVGTTD	HCV NS1 E2 509	93	93
	1283.13	3477	GNWFGCTWMNSTIGET	HCV NS1 E2 550	79	86
	1283.14	3478	FTTLPALSTGLIHLH	HCV NS1 E2 684	79	86
	1283.17	3479	DLYLVTRHADVIPVR	HCV NS3 1134	79	79
	1283.18	3480	RAAVCTIRGVAKAVDF	HCV NS3 1186	79	79
	1283.20	3481	AQGYKVLVLNPSVAA	HCV NS3 1251	79	100
	1283.21	3482	GYKVLVLNPSVAATL	HCV NS3 1253	100	100
	1283.22	3483	VLVLNPSVAATLGFG	HCV NS3 1256	100	100
	1283.23	3484	GTVLDAQETAGARLV	HCV NS3 1335	86	86
	1283.24	3485	GARLVVLAATATPPGS	HCV NS3 1345	79	86
	1283.25	3486	GRHLIFCHSKKKCDE	HCV NS3 1393	100	100
	1283.27	3487	DSVIDCNTCVTQTVD	HCV NS3 1454	86	86
	1283.28	3488	TVDFSLDPTFTIETI	HCV NS3 1466	79	100
	1283.30	3489	FTGLTHIDAHFLSQT	HCV NS3 1567	93	93
	1283.31	3490	YLVAYQATVCARAQA	HCV NS3 1591	79	93
	1283.32	3491	KPTLHGPTPLLYRLG	HCV NS4 1620	79	79
	1283.33	3492	LEVVTSTWVLVGGVL	HCV NS4 1658	86	86
	1283.34	3493	TWVLVGGVLAALAAY	HCV NS4 1664	86	86
	1283.35	3494	AEQFKQKALGLLQTA	HCV NS4 1730	86	86
	1283.40	3495	PAILSPGALVVGVCVA	HCV NS4 1889	79	93
	1283.41	3496	GALVVGVCVAAILRR	HCV NS4 1895	79	79
	1283.42	3497	CAAILRRHVGPGEGA	HCV NS4 1903	79	79
	1283.43	3498	AVQWMNRLIAFASRG	HCV NS4 1917	100	100
	1283.44	3499	MNRLIAFASRGNHVS	HCV NS4 1921	86	100
	1283.48	3500	ANLLWRQEMGGNITR	HCV NS5 2238	86	86
	1283.49	3501	RQEMGGNITRVESIN	HCV NS5 2243	86	86
	1283.52	3502	ARLIVFDLGVRVCE	HCV NS5 2610	79	79
	1283.53	3503	FPDLGVRVCEKMALY	HCV NS5 2615	79	100
	1283.54	3504	GVRVCEKMALYDVVS	HCV NS5 2619	79	100
	1283.56	3505	QPFYDIELITSCSSN	HCV NS5 2808	79	93
	1283.57	3506	LELITSCSSNVSAH	HCV NS5 2813	79	100
	1283.58	3507	PTLWARMILMTHFES	HCV NS5 2870	79	86
	1283.59	3508	LHGLSAFSLHSYSPG	HCV NS5 2919	79	79
	1283.60	3509	AFSLHSYSPGEINRV	HCV NS5 2924	79	79

Table XXXII. Candidate HCV-derived HTL epitopes

Selection criteria	Peptide	SEQ ID	Sequence	Source	Conservancy	
					Total	Core
B. High algorithm conserved core	1283.15	3510	VVLLFLLADARVCS	HCV NS1 E2-724	29	100
	1283.16	3511	SKGWRLLAPITAYAQ	HCV NS3 1025	29	79
	1283.19	3512	PQTFQVAHLHAPTGS	HCV NS3 1225	43	85
	1283.26	3513	DVVVVATDALMTGYT	HCV NS3 1436	43	79
	1283.29	3514	WESVFTGLTHIDAHF	HCV NS3 1563	43	92
	1283.45	3515	LTSMLTDPSHITAET	HCV NS5 2176	57	100
	1283.46	3516	ASQLSAPSLKATCTT	HCV NS5 2208	50	79
	1283.47	3517	DADLJEANLIWRQEM	HCV NS5 2232	50	85
	1283.50	3518	SYTWTGALITPCAAE	HCV NS5 2456	64	79
	1283.51	3519	TTIMAKNEVFCVQPE	HCV NS5 2589	64	85
	1283.55	3519	GSSYGFQYSPGQRVE	HCV NS5 2641	71	79
	1283.61	3521	ASCLRKLGVPPLRVW	HCV NS5 2939	50	85
C. Collaborator	F098.03	3522	AAYAAQGYKVLVLPNSVAAT	HCV NS3 1242-1261	71	100
	F098.04	3523	GYKVLVLPNSVAATLGFAY	HCV NS3 1248-1267	100	
	F098.05	3524	GYKVLVLPNSVAAT	HCV NS3 1248-1261	100	
	F134.01	3525	RRPQDVKFPGGGQIVGGVY	HCV Core 17-35	86	
	F134.02	3526	DVKEPGGGQIVGGVYLLPRR	HCV Core 21-40	86	
	F134.03	3527	GYKVLVLPNSVAATLGFAY	HCV NS3 1253-1272	100	
	F134.04	3528	TLHGPTPLLYRLGAVQNEIT	HCV NS4 1622-1641		79
	F134.05	3529	NFISGIQYLAGLSTLPGNPA	HCV NS4 1772-1791	100	
	F134.06	3530	LLFNILGGWVAAQLAAPGAA	HCV NS4 1812-1831		86
	F134.07	3531	GPGEQAVQWMNRLIAFASRG	HCV NS4 1912-1931	86	100
	F134.08	3532	GEGAVQWMNRLIAFASRGNHV	HCV NS4 1914-1934	100	
	Pape 21	3533	AIPLEVKGGRHLIFCHSKR	HCV NS3 1379-1398	21	100
	Pape 22	3534	GRHLIFCHSKRKCDELATKL	HCV NS3 1388-1407		100
	Pape 29	3535	SVIDC'NTCVTQTVDFSLDPT	HCV NS3 1450-1469	86	
D. DR3 motif	35.0102	3536	GVRVLEDGVNYATGN	HCV 154	86	86
	35.0103	3537	SAMYVGDLCSVTLY	HCV 273	57	86
	35.0104	3538	GHRMAWDMMMNWSPT	HCV 315	86	86
	35.0105	3539	SDLYLVTRHADVIPV	HCV 1133	79	86
	35.0106	3540	VVVVATDALMTGYTG	HCV 1437	42	86
	35.0107	3541	TVDFSLDPTFTIETI	HCV 1466	79	100
	35.0108	3542	DSSVLCFCYDAGCAW	HCV 1518	71	93
	35.0109	3543	GLPVCQDHLEFWEVS	HCV 1552	42	86
	35.0110	3544	GMQLAEQFKQKALGL	HCV 1726	57	86
	35.0111	3545	PTHYVPESDAAARVT	HCV 1936	86	86
	35.0112	3546	GSQLPCEPEPDVAVL	HCV 2162	64	86
	35.0113	3547	LTSMLTDPSHITAET	HCV 2176	57	100
	35.0114	3548	MPPLEGEPGDPDLS	HCV 2401	79	100
	35.0115	3549	QPEYDLELITSCSSN	HCV 2808	79	93
	1283.25	3550	GRHLIFCHSKRKCDEL	HCV NS3 1393-1407		

**Table XXXIV. HLA-DR binding capacity of target derived peptides: DR-supermotif and algorithm positive peptides.**

Peptide	SEQ ID:	Sequence	Source	Binding capacity (IC <sub>50</sub> nM)												DR alleles bound	
				DR1	DR2w2B1	DR2w2B2	DR4w4	DR4w15	DR5w11	DR6w19	DR7	DR8w2	DR9	IAb	bound		
	3551	AAVAAQGYKVI	VI NPSVAAII GFGAY	HCV NS3 1242-1267													
1283.21	3552	GYKVI	VI NPSVAAII	HCV NS3 1253	4.5	350	-	5.2	567	143	5.1	89	288	54	175	9	
1283.20	3553	AGGYKVI	VI NPSVAA	HCV NS3 1251	6.0	650	-	7.9	224	74	5.9	833	175	375	298	9	
198.03	3554	AAVAAQGYKVI	VI NPSVAAI	HCV NS3 1242	2.9	48	483	18	1234	103	11	96	60	240		9	
198.05	3555	GYKVI	VI NPSVAAI	HCV NS3 1248-1261	1.4	39	3695	7.8	141	75	3.5	126	21	266		9	
198.04	3556	GYKVI	VI NPSVAAII GFGAY	HCV NS3 1248-1267	3.5	42	8154	9.7	1500	240	4.1	23	80	20		8	
	3557	GFGAVQWMNRI	IATASRGNIIVS	HCV NS4 1914-1935													
1283.44	3558	MINRI	IATASRGNIIVS	HCV NS4 1921	66	4.8	1538	6329	585	45	7.3	227	102	313	147	8	
1134.08	3559	GFGAVQWMNRI	IATASRGNIIV	HCV NS4 1914	3.2		182	361		345		221	158	6818		6	
1283.16	3560	SKGWR	IATPIAYAQ	HCV NS3 1025	0.36	125	23	24	152	4.8	-	962	54	1190	384	8	
1283.55	3561	GSSYGHQYSPGQRVE		HCV NS5 2641	11	-	667	417	745	20000	19	156	-	68	571	7	
1283.61	3562	ASGTRKI	GVPPIRVW	HCV NS5 2939	5.0	16	217	6250	78	645	2500	802	671	8621	-	7	
1134.05	3563	NIISGHIQYI	AGLSHLPGNPA	HCV NS4 1772	10		606	84		29		-	70	441		6	

Shading indicates IC<sub>50</sub> < 1 μM

A dash (-) indicates IC<sub>50</sub> > 20 μM

Table XXXV. HLA-DR binding capacity of 3 DR3 motif-containing peptides

Peptide	Seq #	Sequence	Source	DR3 binding* (IC <sub>50</sub> nM)
35.0106	3564	VVVVATDAlMTGYTG	HCV 1437	427
35.0107	3565	TVDFSLDPTFTIETT	HCV 1466	235
1283.25	3566	GRIILIFCTISKKKCDE	HCV NS3 1393	ND

Table XXXVIa: HCV-derived CTL epitope candidates

Peptide	Molecule	1st Position	Seq ID	Sequence	Consv.	Selection criteria
1073.05	NS4	1812	3567	LLFNILGGWV	85	A2-supertype
1090.18	NS1/E2	728	3568	FLLADARV	92	A2-supertype
1013.02	NS4	1590	3569	YLVAYQATV	85	A2-supertype
1090.22	NS5	2611	3570	RLVFPDLGV	79	A2-supertype
1013.1002	CORE	132	3571	DLMGYPLV	79	A2-supertype
24.0073	NS4	1920	3572	WMNRLIAFA	100	A2-supertype
24.0075	NS4	1666	3573	VLVGGVLA	85	A2-supertype
1174.08	NS4	1769	3574	IIMWNFSCI	92	A2-supertype
1073.06	NS4	1851	3575	ILAGYGAGV	79	A2-supertype
1073.07	CORE	35	3576	YLLPRRGPR	92	A2-supertype
24.0071	NS1/E2	726	3577	LLFLLADA	100	A2-supertype
1.0119	LORF	1131	3578	YLVTRIADV	85	A2-supertype
1.0952	CORE	51	3579	KTSESRQPR	92	A3-supertype
1073.11	CORE	43	3580	RLGVRATRK	79	A3-supertype
1.0955	ENV1	290	3581	QLFTESPRR	79	A3-supertype
1073.13	NS1/E2	632	3582	RMVVGVEHR	100	A3-supertype
1.0123	NS3	1396	3583	LIFCHSKKK	100	A3-supertype
1073.10	NS4	1863	3584	GVAGALVAFK	85	A3-supertype
24.0090	NS4	1864	3585	VAGALVAFK	85	A3-supertype
24.0086	NS3	1262	3586	TLGFGAYMSK	85	A3-supertype
F104.01	NS5	3003	3587	VGIYLLPNR	79	A31
1145.12	Core	169	3588	LPGCSFSIF	92	B7-supertype
29.0035	NS3	1378	3589	IPFYGKAI	92	B7-supertype
13.0019	NS5	2922	3590	LSAFSLHSY	79	A1
1069.62	NS3	1128	3591	CTCGSSDLY	79	A1
24.0092	NS4	1765	3592	FWAKIMWNF	85	A24

Table XXXVIIb. HCV-derived HTL epitope candidates

Region	Peptide	Motif <sup>1</sup>	Seq ID	Sequence
HCV NS3 1025-1039	1283.16	DR	3593	SKGWRLLAPITAYAQ
HCV NS3 1242-1267	F98.03	DR	3594	AAVAAQGYKVLVLNPSVAAT
HCV NS3 1393-1407	1283.25	DR3	3595	GRHLIFCHSKKKCDE
HCV NS3 1437-1451	35.0106	DR3	3596	VVVVATDALMTGYTG
HCV NS3 1466-1480	35.0107	DR3	3597	TVDFSLDPTFTIETT
HCV NS4 1772-1790	F134.05	DR	3598	NFISCIQYLAGLSTLPCNPA
HCV NS4 1914-1935	F134.08	DR	3599	GEGAVQWMNRUIAFASRGNIHV
HCV NS5 2641-2655	1283.55	DR	3600	GSSYGFQYSPGQRVE
HCV NS5 2939-2953	1283.61	DR	3601	ASCLRKLGVPPLRVW

1. Peptides identified on the basis of either the DR P1-P6 supermotif or by use of the DR1-4-7 algorithms are indicated by 'DR'. Peptides identified using the DR3 motif are indicated by 'DR3'.



Table XXXVII. Estimated population coverage by a panel of HCV derived HTL epitopes

Antigen	Alleles	Representative assay	No. of epitopes <sup>2</sup>	Population coverage (phenotypic frequency)					
				Cauc.	Blk.	Jpn.	Chn.	Hisp.	Avg.
DR1	DRB1*0101-03	DR1	6	18.5	8.4	10.7	4.5	10.1	10.4
DR2	DRB1*1501-03	DR2w2 B1	3	19.9	14.8	30.9	22.0	15.0	20.5
DR2	DRB5*0101	DR2w2 B2	6	-	-	-	-	-	-
DR3	DRB1*0301-2	DR3	2	17.7	19.5	0.40	7.3	14.4	11.9
DR4	DRB1*0401-12	DR4w4	5	23.6	6.1	40.4	21.9	29.8	24.4
DR4	DRB1*0401-12	DR4w15	3	-	-	-	-	-	-
DR7	DRB1*0701-02	DR7	5	26.2	11.1	1.0	15.0	16.6	14.0
DR8	DRB1*0801-5	DR8w2	5	5.5	10.9	25.0	10.7	23.3	15.1
DR9	DRB1*09011,09012	DR9	3	3.6	4.7	24.5	19.9	6.7	11.9
DR11	DRB1*1101-05	DR5w11	5	17.0	18.0	4.9	19.4	18.1	15.5
DR13	DRB1*1301-06	DR6w19	2	21.7	16.5	14.6	12.2	10.5	15.1
Total <sup>1</sup>				98.5	95.1	97.1	91.3	94.3	95.1

1. Total population coverage has been adjusted to account for the presence of DRX in many ethnic populations. It has been assumed that the range of specificities represented by DRX alleles will mirror those of previously characterized HLA-DR alleles. The proportion of DRX incorporated under each motif is representative of the frequency of the motif in the remainder of the population. Total coverage has not been adjusted to account for unknown gene types.

2. Number of epitopes represents a minimal estimate, considering only the epitopes shown in Table 6. Additional alleles possibly bound by nested epitopes have not been accounted.